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Database
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        otal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A_Geneseq_101002:*

1: /SIDS2/gcgdata/ge
2: /SIDS2/gcgdata/ge
3: /SIDS2/gcgdata/ge
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            March 28, 2003, 13.21.54; Search time 81 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         นบัฟ470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gapop 10.0 , Gapext 0.5
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           Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                         /SIDS2/qcgdata/qeneseq/geneseqp-embl/AA1987.DAT:*
/SIDS2/qcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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/SIDS2/gegdata/genesed/genesedp.embl/AA2000.DAT.*
/SIDS2/gegdata/genesed/genesedp.embl/AA2001.DAT:*
/SIDS2/gegdata/genesed/genesedp.embl/AA2001.DAT:*
                                                                                                                                                                                                                                                                                                                                        /SIDS2/gcgdata/gcncseq/geneseqp-embl/AA1989.DAT:*
/SIDS2/gcgdata/geneseq/gencseqp-embl/AA1990.DAT:*
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1979.018 Million cell updates/sec
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUM	
MAR	
ES	

Result.		Query				
No.	Score		Leagth	DB	TD.	Description
1	6294		1203	tu tu	AAM52633	Varicella-Foster v
2	3016.5	47.9	1196	19	AAW72105	HSV-2 strain SB5 C
نبا	1566.5	24.9	623	19	AAW72197	HSV-2 strain SB5 C
4	1380.5	21.9	543	19	AAW72196	HSV-2 strain SB5 C
5	620	<u>و</u> . و	1132	tu F=	AAB53126	Macaca mulatta rha
6	183	2.9	35	20	AAY26935	Varicella zoster v
7	183	2.9	35	22	ААН73931	Varicella zoster V
œ	156.5	2.5	1841	2	AAHU7562	Protein encoded by
9	123.5	٠.٠	3210	t.	AAB73958	Myselia sterilia s
10	123	: J	1074	ر د	AAY00205	Enterococcus faeca

Composition of matter for delivering desired compounds into eukaryotic rell, comprises Varicella-2oster virus open reading frame 29p protein either bound to an agent or operably affixed to lipid-soluble group .

Precursor mutant C		14	774	1.6	103	4
Novel human diagno	2 ABG21521	22	1750	1.6	103.5	44
flg receptor prote		1	821	1.7	104	43
Cephalosporin C ac		16	774	1.7	104	42
Sequence encoded b		13	774	1.7	104	41
Human protein sequ		22	3530	1.7	104.5	40
Rat CIRL-1 variant		23	1515	1.7	104.5	39
Calcium independen		19	1471	1.7	104.5	ω 8
Trp168Tyr cephalos		18	774	1.7	105	37
eryA region polype		14	3567	1.7	106.5	36
Human dachsous pro	3 ABB05430	23	3298	1.7	106.5	35
Novel human diagno	2 ABG07171	r) Ci	794	1.7	106.5	34
Cephalosporin C ac		16	774	1.7	106.5	S S
A splice variant o		22	2596	1.7	1 Ü B	ندا
Human protein segu		22	1451	1 7	108.5	درا دیو
Streptomyces nours		ri Ci	11096	1.7	109	Ü.
Mycobacterium tube		E3	3070	1.8	110.5	29
Drosophila melanog		ts ts	1532	1.8	110.5	83
S. venezuelae vep		:2	4630	1.8	111	27
Streptomyces venez		18	4630	1.8	111	26
Cephalosporin C ac	⊳	7	774	1.8	114	25
Human peroxidasin		t)	1498	1.8	114.5	13 4
Human p53 target m		21	1496	1 8	114.5	S S
Melanoma associate	0.5018MVV	20	1496	1.8	114 5	IJ
Ge protein fragmen	AAR43950	14	1150	1.8	115	21
Nevel human diagno		1-1 1-1	1784	1.9	118	2
Novel human diagno		10 10	1076		118.5	19
Pat OCP Pattus r		r.	2597	1.9	120.5	ω
Mechanical stress		21	2597	1.9	120.5	17
Human OPFX OPF1700		13	1069		121	16
Mechanical stress		21	2387		122.5	5
Drosophila melanog		E E	901	1.9	122.5	14
E factalis EF102 p		23	1074		123	<u>.</u>
E faecalis EF094 p		د ا س	1074	ນ . 0	123	5
Enterococcus laeca	88100 YAA	20	1074	ນ 0	123	11

ALIGNMENTS

RESULT 1 ORF29p; open reading frame 29p protein; Varicella: Zoster virus; VZV; drug delivery, gene delivery; fusion protein; protein secretion. AAM52633 standard; Protein; 1203 AA Varicella-Zoster virus (VZV) ORF29p protein 18-FEB-2002 (first entry) Silverstein S, Annunziato P, (HYCO) UNIV COLUMBIA NEW YORK. 25-JAN-2000; 2000US-0177901 25-JAN-2001; 2001WO-US02500. 02-AUG-2001. W0200154709-A1. Human herpesvirus 3. AAM52633; N-PSDB; 2001-488744/53. DB; ABA02175. Gershon A, Lungu o:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents the Varicelia-Zoster virus (VZV) open reading trame 29p (ERF29p) protein. Although orR29p is the major DNA binding protein or VZV, the invention is based on the discovery that the VZV orF29p protein can readily enter and exit eukaryotic cells. Accordingly, the invention relates to a composition for delivery of an agent into a eukaryotic cell. Comprising the VZV OrF29p protein bound to the agent into a eukaryotic cell. Comprising the VZV OrF29p protein bound to the agent to be delivered. The agent delivered may be a polypeptide, a polymericotide, or an organic compound. The invention also relates a composition in which the OrF29p protein is linked to a lipid membrane, and lipid vesicles containing this composition. The invention additionally relates to the use of the OrF29p protein as a facilitator of secretion of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a desired protein, in which the desired protein and the ORF29p protein are tremmbliantly expressed as a fusion protein. The invention further encompasses nucleic acids encoding the VZV OFF29p protein and their use in detection of VZV OFF29p nucleic acids, and a monoclonal antibody adainst the ORF29p protein. Compositions of the invention are useful for the delivery of a prophylatetic or therapeutic agent to a cokaryctic cell, particularly a human cell. Examples of agents that can be delivered to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antineoplastic, antidiabetic or immunosuppressive drugs).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cell include proteins such as insulin, factor VIII, factor IX, and proteases: polynucleotides (e.g., for use in gene therapy), and organic compounds such as vitamins and a wide variety of pharmaceutivals (e.g.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Fig 6; 68pp; English.
541 YSBCDPLGNYAPYLILRKPGDQTEAAKATMQDTYRATLERLFIDLEQERLLDRGAPCSSE 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 VIAPMAVALRYRNYTAVARGAAHLAFDENHEGAVLPPDITYTYFQSSSSGTTTARGARRN
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                                                                                                                                                                                                                                                                                                                                                                                                            461 KINALGSYTARVAGVIGAMVESPNSALYLTEVEDSGMTEAKDGGPGPSFNRFYQFAGPHL 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24) VIAPMAVALRVRNVTAVARGAAHLAFDENHEGAVLPPDITYTYFQSSSSGTTTARGARRN 300
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                                                    YSDODPLGNYAPYLILEKFGDOTEAAKATMODTYRATLERLFIDLEQEELLIDEGAPCSSE 600
                                                                                                              GUALKYYTGTFDSEIPCSLCEKHTRPVCAHTTVHRLRQRMPRFGQATPQPIGVFGTMNSQ
                                                                                                                                                                            GDALKYVTGTFDSEIPCSLCEKHTRPVCAHTTVHRLRQRMPRFGQATRQPIGVFGTMNSQ 540
                                                                                                                                                                                                                                                                                                                                                  RLNALGSYTARVAGVIGAMVESENSALYLTEVEUSGMTEAKLGGEGESENREYQEAGEHL
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                                                                                                                                                                                                                                                               AANPQTDRDGHVLSSQSTGSSNTEFSVDYLALICGFGAPLLARLLFYLERCDAGAFTGGH 480
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                                                                                                                                                                                                                                      AANPOTDRIGHVI.SSOSTGSSNTEFSVDYLALTCGFGAPLLARILFYLERCDAGAFTGGH
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                                                                                                                                                                                                                                                                                                                                                                                 1203 AA;
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100.0%; Pred. No. 0;
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                Chan JY,
                                                                                                        09-JIIN-1997;
                                                                                                                                                                                                                                                                           HSV-2 strain SB5; immunological response induction, therapy; antiviral identification; viral protein inhibitor.
                                                                                                                                                                                                                                                                                                                                  HSV-2 strain SB5 Contig ID 12 ORF#2 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW72105 standard; Protein; 1196 AA
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                                                                                       04-NOV-1996;
                                                                                                                                         31-OCT-1997;
                                                                                                                                                                                                             W09820016-A1
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                                                 (SMIK ) SMITHKLINE BEECHAM CORF.
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                  Dabrowski-Amaral CE,
Leary JJ
                                                                                                          97115-0049018
                                                                                       96US-0030279
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                  Delvecchio AM, Dillon SB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a Herpes simplex virus type-2 (HSV-2) protein sequence of the invention. This sequence was isolated from a HSV-2 strain SB5 (deposited as ATCC VK-2546) LNA fragment designated Courty ID 12. The proteins can be used for the treatment or prevention of disease, to induce an immunological response in a mammal or to identify inhibitors, activators or novel antivirals. Antagonists of the proteins can be used to inhibit a viral polypeptide. The DNA sequence or a vector containing it can also be used to induce an immunological response in a mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 10; Page 83-84; 748pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAV62156
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655 SESEDPYTGJPGPELQELAKRSNEAVYQDEALSQCHGVFAGQSVEGRNFRNQFQPVERRR 714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 TTTTVKVPPGPMGYYYGRACPAEGLEL--LSLLSARSGDADVAVAPLIVGLTVESGFEAN 64
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                                                    ALTEDPYSGAFCPLTNFLVKRTHLAVVODLALSOCHCVFYGQQVEGRNFRNQFQPVLKKR 713
                                                                                                         AVPTALGRLETIIGTREALHTVVNNIKQLVDREVEQLMRNLIEGRNFKFRDGLAEANHAM 654
                                                                                                                                                         GAPCSSEGLSSVIVDHPTFRRILDTLRARIEQTTTQFMKVLVETRDYKIREGLSEATHSM
                                                                                                                                                                                                                                                                                                                    VIVGRQEMDVEKYVADSGQTDVPCNLCTFETRHACAHTTLMRLRAPHPKFASAAFGAIGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LNALGSYTARVAGVIGAMVFSPNSALYLTEVEDSGMTEAKDGGPGPSFNRFYQFAGPHLA 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HINHADVIRIPLEPVQLEMPDVNRLVPDPENTHHRSIGEGEVYPTPEYNTGIALIHDAV 241
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                                                                                                                                                                                                                FIGUMNSAYSUCUVLIGNYAAFSALKK-AUGSENTKT IMQETYKAATEKVMAELEALQYVUQ
                                                                                                                                                                                                                                                                  FGTMNSQYSOTOPIGNYAPYLTLFKFGDQTEAAKATMQDTYRATLEFLFIDLEQERILDF 593
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RESULT 3
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                mammal
                                Herpes simplex virus type-2 sequences—useful in, e.g. prevention and treatment of infection or inducing immunological response in
                                                                                                                                                                                                                                          09-JUN-1997;
04-NOV-1996;
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                                                                                          N-PSDB; AAV62176.
                                                                                                                                                                                                                                                                                                  31-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      antiviral identification; viral protein inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSV-2 strain SB5; immunological response induction; therapy;
                                                                                                            WPI; 1998-286847/25
                                                                                                                                                  Esser KM,
                                                                                                                                                                                                      (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSV-2 strain SB5 Contig ID 15 ORF#32 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LUEKTTAGUGETPTNLAFNFUSCEPSHUTTSNVLNISGSNISGSTVPGLKKPPEDDELFU 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TVKSLGPRTQQLQIEDWLALLEDEYLSEEMMEFTTRALERGHGEWSTDAALEVAHEAEAL 1131
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                                                                                                                                                                  Dabrowski-Amaral CE,
                                                                                                                                              Leary JJ;
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                                                                                                                                                                    Delvecchio AM,
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RESULT: 4
AAW72196
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                          HSV 2 strain SB5 Contiq ID 15 ORF#31 protein.
                                                                                    13 JAN 1999
                                                                                                                                                                                             AAW72196 standard; Protein; 543 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                activators or novel antivirals. Antagonists of the proteins can be used to inhibit a viral polypeptide. The DNA sequence or a vector containing it can also be used to induce an immunological response in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents a Herpes simplex virus type 2 (HSV 2) protein sequence of the invention. This sequence was isolated from a HSV-2 strain SH5 (deposited as AICC VR-2546) by trainent designated Contig ID 15. Based on homology, this sequence is a major DNA-binding protein. The proteins can be used for the treatment or prevention of disease, to induce an immunological response in a mammal or to identify inhibitors,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                          595 VPTALGREETIIGTREALHTVVNNIK 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       535 GTMNSQYSOCOPIONYASYLILEKPGDQTEAAKATMQDTYFATLERLEIDLEQERLLDRG 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                476 FTGGHG DALKYVIGTEDSETPCSICEKHTRPVCAHTTVHRLRQRMPRFQQATRQPIGVF 534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTMNSAYSINODVIGNYAAESALKK-ADGSENTRITIMQETYRAATERVMAELEALQYVDQA 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TVGRQEMDVERYVADSGQTDVPCNLCTFETRHACAHTTLMRLRARHPKEASAARGATGVF 535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NSTSKPSPSGGFERRLASIMAADTALHAEVIENTGIYEETPTDIKEWPMFIGMEGTLPRL 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APMAVALRYRNYTAVARGAAHTAFDENHEGAVLPPDTTYTYFQSSSSGTTTARGARRNDV 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IGDAEVHRIDVYPLOMEMPDESEVIADDENCNHKSIGENENYDDEENRDLARLLEEAVV 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SBYAFRPCDLKHETFODALGERLGI,DFDRALLYLV FFEGFREAVG I SNTFLHLGGMDKVT 184
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                                                                                 (tirst entry)
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1072 TVVRAVGARAQHMAFDDWLSLTDDEFLARDLEELHDQIIQTLETPWTVEGAL - - - EAVK 1127

1012 NVCPLETEDRIRREITACPRGGFTCPVTGPSSGNRETTLSDQVRGITVSGGAMVQLATYA 107

SLDAHPGAWTSMFASCNLLRPVMAARPMVVLGLSISKYYGMAGNDRVFQAGNWASLLGGK 357

713 REVDLENGGEISTESITYTLSEG-PVSAPNPTLGQDAPAGRTFDGDLARVSVEVIRDIRV 771

61 RVMDLENNGELSAKTLITVALSEGAATCAPSLITAGQTAPÄESSEEGDVARVILGEPKELRV 120

KSRVLFAGASANASEAAKARVASLQSAYQKFDKRVDILLGPLGFLLKQFHAVIFPNGKPP 180 KNRVVESGNCTNLSEAARARLVGLASAYQRQEKRVDMLHGALGELLKQEHGLLEFFRGMPF 831

358 NACPILLEDRIPKEVI.ACPRAGEVCAASSIGGGAHEHSLCEQLEGITAEGGAAVASSVEV 417

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Matches
                                                                                                          Query Match
                                                                                                                                                                          sequence of the invention. This sequence was isolated from a HSV 2 strain SB5 (deposited as ATCC VR-5346) LNA fragment designated Contig ID 15. Based on homology, this sequence is a major DNA-binding protein. The proteins can be used for the treatment or prevention of disease, to induce an immunological response in a mammal or to identify inhibitors, activators or novel antivitals. Antagonists of the proteins can be used to inhibit a viral polypeptide The DNA sequence or a vector containing it can also be used to induce an immunological response in a mammal.
                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                             Claim 10, Page 122:123; 748pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Herpes simplex virus type 2 sequences .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Esser KM,
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                                                                                                                                                                                                                                                                                                                            This sequence represents a Herpes simplex virus type-2 (HSV-2) protein
                                                                                                                                                                                                                                                                                                                                                                                                                     and treatment of infection or inducing immunological response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-286847/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SMIK ) SMITHKLINE BEECHAM CORP
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                                653 MALITFOPYSGAFGPITNFLYKKTHLAVVQDLALSQCHCVFYGQQVEGKNFRNQFQPYLKR 712
                                                                       Local Sin
hes 271;
1 MSLSLDPYTCGPCPLLQLLARRSNLAVYQDLALSQCHGVFAGQSVEGRNFRNQF@PVLRR 60
                                                                                        Similarity
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                                                                                                                                           543 AA;
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                                                                       Conservative
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                                                                   21.9%; Score 1380.5; DB 19; Length 543; 48.7%; Pred. No. 3.4e-125; ative 101; Mismatches 165; Indels 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Delvecchio AM,
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genome; Kaposi's sarcoma-associated herpesvirus; KSHV; interleukin 6; IL-6, macrophage inflammatory protein; MIP, diagnosis, vaccine, cytostatic; anti-HIV; gene therapy; infection; KAposi's sarcoma, lymphoproliterative disorder; B-cell hyperplasia; lymphadenopathy; splenomegaly; hypergammaglobinulinaemia; autoimmune haemolytic anaemia.
associated with RRV infection. It is also useful for testing the efficacy of the candidate vaccine against RRV infection or conditions associated with its infection by administering the vaccine to the subject with RRV and observing the effect of vaccine. AAC64755 to AAC64765 and AAB53205 to AAB53213 represent sequence used in the exemplification of the
                                                                                                                                  administering the drug to a immuno-compromised non-human primate pretrably knesus macague monkey obtained by as a result of infection by simian immunodeficiency virus (SIV). KRV is useful for producing non-human primate model for testing potential treatments for conditions
                                                                                                                                                                                                                              disorders, B-cell hyperplasia, lymphadenopathy, splenomegaly, hypergammaglobinulinaem.a or autoimmune haemolytic anaemia, b
                                                                                                                                                                                                                                                                                                                                                             encoded by the genome sequence. The present invention also specifically claims the individual open reading frame (ORF) nucleotide sequences from
                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a novel rhesus maraque rhadinovirus called macaca mulatta rhadinovirus 17577 (RRV) AAC64754 represents the RRV genome sequence, and AAB53123 to AAB53204 represent the proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5; Page 123; 141pp; English.
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                                                                                                                                                                                                                                                                      infection with RRV such as Kaposi's sarcoma, lymphoproliferative
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                                                                                                                                                                                                                                                                                         genome which encode the individual proteins, but these sequences are given. A non-human animal infected with RRV can be used for testing efficacy of drug in the treatment of condition associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rhesus rhadino virus for producing non-human primate model useful testing potential treatments and efficacy of the candidate vaccine conditions associated with RRV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               conditions associated with RRV infection
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                                                                                                                                 RILESN--FAGSEAVQSGFVKFTGTRDTY-----VVAGFYMKFLNSLHKALF----
                                                                                                                                                                            RVVFSGNCTNLSEAARARLV---GLASAYQRQEKPVDMLHGALGFLLKQFHGLLFPRGMP
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                                                                                     PNSKSPNPQWFWTLLQRNQMPADK-LTHEEITTIAA-VKRFTEEYAAINFINLPPTCIGE
                                                                                                                                                                                                                                                                   ----NGGF ISTRSTTVTLSEGPVSAPNPTLGÓDAPAGKTFDGDLARVSVEVIRÐIRVKN
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22.6%; Fred. No. 1.7c-50;
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                                                               transposase molecules. The poptides, or their homologues, have the rollowing identifying characteristics: (a) an initial and terminal amino acid comprising Asp or GIU, separated by 34-39 amino acids (the D3SE motil): (b) a high probability \{p<0.05\} of alignment with a consensus sequence (AAV26941), as determined by:
the homologue with those of the consensus by maintaining the spacing of
                                                                                                                                                                              The invention relates to movel recombinogenic motils found in (retro)viral integraces which have similarity to invertebrate
                                                                                                                                                                                                                                                  Claim 1: Column 37 38; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinogenic motil: retrovirus; integrase; invertebrate; transposase; conscuss; vaccine; gene therapy; allergy; autoimmune disease; cancer; cardiovascular disease; graft rejection; hematopoletic disorder; immunosuppressive disorder, immunoproliferative disease; jaundice; immunodeliciency disease; intectious disease; inflammatory disease; septic shock; metabolic defect.

    aligning the initial and terminal residues of the homologue sequence
with those of the consensus;
    aligning the intersening residues of

                                                                                                                                                                                                                                                                                             production of vaccines and in dene therapy
                                                                                                                                                                                                                                                                                                                Peptides derived from a Herpes virus recombinogenic motif useful for the
                                                                                                                                                                                                                                                                                                                                                                    WP1: 1999 561074/47
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02 AUG 1996;
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               encoding a peptide consisting of one of ten amino acid sequences defined in the specification or homologues of these sequences. The nucleic acid molecules are useful for producing peptides important in the regulation and function of herpes virus replication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the consensus while, if necessary, altering (by the insertion of spaces or the deletion of residues) the spacing of the homologue; and (3) generating a distribution of 1500 random sequences of amino acids between the initial and terminal residues and identifying the percentage of aligned residues. The recombinogenic motifs may be useful in the production of vaccines and in gene therapy to treat allergies, autoimmune diseases, cardiovascular diseases, graft rejection, the contents of the co
                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid molecules encoding peptides with transposase activities, useful as immunosuppressants, anti-viral agents, or vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Varicella zoster virus; VZV29; herpesvirus; D35E; anti-viral; immunosuppressant; immunostinulant; cytostatic; anti-allergic; cardiant; anti-inflammation; gene therapy, infection, herpes virus repileation; anti-inflammation; retroviral integrase; (VD)J recombination; retroviral integrase; fimmunoglobulin class switching; allergy; autoimmune disease; cancer; cardiovascular disease; graft rejection; haematopoietic disorder; cardiovascular disease; graft rejection;
                                                                                                                                                                 The present sequence is provided in a specification relating to a isolated nucleic acid molecule comprising a nucleic acid sequence
                                                                                                                                                                                                                                                                              Claim 1; Column 25, 31pp; English.
                                                                                                                                                                                                                                                                                                                                                      cancers or graft rejection
                                                                                                                                                                                                                                                                                                                                                                                    for gene therapy of diseases, e.g. allergies, autoimmune diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-256131/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dreyfus DH, Gelfand
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02-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Varicella-zoster virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Varicella zoster VZV29 protein recombinogenic sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-MAY-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hematopoietic disorders, immunosuppressive disorders, innectious immunoproliferative diseases, immunodeficiency diseases, intectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diseases, inflammatory diseases, jaundice, septic shock and other immunological, genetic or metabolic detects.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunological disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     545 DPLGNYAPYLILRKPGDQTEAAKATMQDTYRATLE 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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960S-0023064
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Pred. No. 3.1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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Y(D)J recombination,

retrovitai integrase function or immunoglobulin

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AAHU7562
Query Match
Best Local :
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                                                                                                                                       8 to 30 of the BLM (Bleomycin) gene cluster. The proteins encoded by the gene cluster are useful for producing peptides and/or polyketide metabolites, especially bleomycin or bleomycin analogues. They are also useful for chemically modifying biological molecules to produce
                                thiazolidine, thiazoline, bithiazoline and bithiazoline-containing microbial metabolites. The BLM gene cluster may also be used to pr
                                                                 branched methyl groups, and for coupling amino acids and fatty acids. They may be reacted with an apo-carrier protein and coenryme A to produce a holo-carrier protein. The BLM gene cluster or catalytic domains can be used individually or collectively to produce
                                                                                                                                                                                                                AAB07556-78 represent proteins encoded by open reading frames (ORFs)
                                                                                                                                                                                                                                                     Disclosure; Page 97-137; 162pp; English.
                                                                                                                                                                                                                                                                                          chemically modifying biological molecules
                                                                                                                                                                                                                                                                                                           New bleomycin gene cluster components useful for peptide and/or polyketide metabolites, especially bleomycin, production and for
                                                                                                                                                                                                                                                                                                                                                                     N-PSDH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thiazoline; bithiazoline, microbial metabolite, sugar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bleomycin, bleomycin analogue, holo carrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BLM gene cluster; bleomycin gene cluster; polyketide metabolite;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein encoded by the bleomycin (BLM) gene cluster ORF30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB07562 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genetic or metabolic defects.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   class switching. The isolated nucleic acid molecules and the peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       545 DPLGNYAPYLILRKPGDQTEAAKATMQDTYRATLE 579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             461 PMPLVVSAKTKEALAEAVRULAAWSAPEPGTKLADLAATLAGKKAFPYRAAVVCHDLPEA 520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                    GKRDVGTWCYARGWRHAAPADPAPLTGGCLLLGDGDTAKAVASRI.E··ALGV!'VTTVGGG 129
                                                                                                                                                                                                                                                                                                                                                                                          YRATLERLFI-------DLEQERLLDRGAPCSSEGLS-----SVIVDHPT 611
                                                                                                                                                                                                                                                                                                                                                                                                                                        TRLAGSLLDRLAADREPGRPLRVLEAGAG----AGSLTQALVTRAPG-----RLDY 1073
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                                         APAG----RIFUGDLARVSVEV--IRDIRVKNRVVFSGNCTNI.SEAARARLVGLASAYOR 801
                                                                                                                                                                         WHHTDRRTHGPLLDAAGWRALLAGEDFATADVIVPPDGPQDAALLLARQTPRPAAAAPSV
                                                                                                                                                                                                                                                                                                        FRRILDTLRARIEQTTTQFMKVLVETRDYK1REGLSEATHSMALTFDPYSGAFCPIT---
                                                                                                                                                                                                                                                                                                                                                 HATDISRHEVTALGREAAKRGLUEVRAKVLUIAKUPGEQGFAGEKFUVVCGLUVVHATPD 1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YPRALSTPGAALDVLYPAGSGDLLRRTLG-------EGTADHRATGRL 1026
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NDVN----STSKPSPSGGFERRLAS------IMAADTA---LHA-EVIFNTGIY-
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                                                                                                                                PRRFVDLF-----
                                                                                                                                                                                                                                                              LRTTLGHLRSLMAPDGT - - - LALIET -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRFG-----QATRQPIGVFGTMNSQYSDCDPLGNYAPYLILRKPGDQTEAAKATMQDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -GTLPRLNALGSYTARVAGVIGAMVFSPNSALYL-TEVEDSGMTEAKDGGPGPSFNRFYQ 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -SGAR-TTGLAGAGITLKLTTSHFYPSVFVFHGGKHVLPSSAAPNLTRACNAARERF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1841 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----EWPMFIGME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -DACAECFAPLGTDLHAALGAPADDT---RAAQPALFAVEYALARTLMDWGV 615
                                                                                                                                                                                                                   -----LAVVQDLALSQCHCVFYGQQVEGRNFRNQ-----FQPVL 710
                                                                                                                                ----STRSITVTLSEGPVSAPNPTLGQD
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19.6%; Fred. No. 0.00013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      470;
                                                                                                                                                                                                                                                              ---TADDPWLTMIWGLTDGW 1173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --PSFSGLVDLLRHCAQG
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    Querry Match
                                                                                                                                                                 The present sequence is a cyclic depsipeptide synthase from Mycelia sterilia. The present protein, or a protein containing an addition, deletion and/or substitution of one or more amino acid residues is useful for the efficient production of the anthelmintic PF1022 (cyclo(D-lactyl-L.N methylleucyl D + phenyllactyl-L-N-methylleucyl-D-lactyl-L-N-methylleucyl-D-3 phenyllactyl-L-N-methylleucyl-D-3.
                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 59-80; 92pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel cyclic depsipeptide synthase and gene encoding it for efficient production of anthelmintic substance {\tt PF1022}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N PSDB; AAF79702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Midoh N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MEIJ ) MEIJI SEIKA KAISHA JID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07 SEP 1999; 99JP-0253040;
96 APP-2000; 2000JP 0104291.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycelia sterilia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycelia sterilia cyclic depsipeptide synthase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH/3958 standard; Protein; 3210 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1566 AGMIQRRDRAGTDAALAAKLTGTL-----VLDEVFAHRDLDFL 1603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   137/ HPEHATVPAAAKVIPREYPWIACTALDVEPGLDAE----RLADLIVRELGAAR---ETTV 1429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1352 LEERHPARVVTVTTGA-----HDVL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycelia sterilia; cyclic depsipeptide synthase; anthelmintic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 MAY 2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1063 -AMVQLATYATYVKAVGARAQHMAFDDWLSLTDDEFLARDLEEL 1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102 + RRETIACPRGGETCPVTGPSSGNRETTLSDQ------VBGITVSGG---- 1062
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Futamura T,
                                                                                         3210 AA;
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F, Kleinkauf H,
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    Score 123.5;
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DB 22;
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Length 3210;
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                                                                                                  14-NOV-1997;
06-MAY-1997;
16-MAY 1997;
                   Bailey C,
                                                           (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                       U4-MAY-1998;
                                                                                                                                                                                                                                                                                                                 Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY00206,
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                                                                                                                                                                                                                                 12-NOV-1998
                                                                                                                                                                                                                                                                        W09850554-A2
                                                                                                                                                                                                                                                                                                                                                         detection; attenuation;
                                                                                                                                                                                                                                                                                                                                                                          Enterococcus faecalis; infection; vaccine; immune response; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                  Enterococcus faecalis protein EF102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2779 QLQCSPETILDVYPATQMQRVFLLNPVTGKPRSPTPFHIDFPPD-----ADCASLMRAC 2832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2631 - PVISDLAVTLP@GLTLENALFATEDSGYWEQTMSAFTIFSDDMEAVDJKEFALVLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2550 RRAYLAPKSYAAPA-----KPVKYVDFFVNLEAIL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            466 FYLERCDAGAFTGGHG------DALKYVTGTFDSE1PCSLCEKHTRPVCAHT 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        758 LARVSVEVIRDIRVKNRVVFSGNCT -----NLSHAARARLV----GLASAYQ 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      603 SSVIVDHPTERRILDTLRARIEQTTTQFMKVLVETRDYKIREGLSEATHS----- 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          357 GTLPRINALGSYTARVAGVIGAMVFSPNSALYLTEVEDSGMTEAKDGGPGPSFNRFYQFA 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                298 RRNDVNSTSKPSPSGGFERRLASIMAADTALHAEVIENTGIYEETPTDIKEWPMFIGME- 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PKFAGYMOHVASSRREGYDFWR-SVLRDSSMTVIKGNNNTTPPPPPQQQSTPSGAHHASK
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                   Choi GH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 9; Page 197-198; 3ulpp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated Enterococcus faecalis polynucleotides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus infection {\sf Constant}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Products from the present invention can also be used for screening compounds to identify agenists and antagonists of {\tt E}. faecalis protein
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                                                                                                                                                                                                                                                                                                                                       474 NQETTGETTUTKEDKDTGNESQGKAEFKGAEYTLFTAKDGQAVKWSEAFK-----TEL 526
                                                                                                                                                                                                                                                                                                                                                                                             676 HIAVVODIAL------SQCHCVFYGQQV------EGRNFRNQFQPVLRRRFVDL 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                         418 RAE--TPKELANALELGTYYVTE--TKSSNGFVNTFKPTKVELKYANQTVALVTSNVKGQ 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              622 RIEGTTTGEMKVLVETRDYKIREGLSEATHSMALTFDP-----YSGAFGPITNFLVKRT 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    359 SMTSKNMRQKGQILLEKTG-VETGTDLWNDNYSLAGNTFAIRKDSPAGEIVQEITTDEKG 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             571 QDTYRATLERLFIDLEQERLLDRGAPCSSEGLS-----SVIVDHPT---FRRILDTLRA 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     305 ALPSKDVTTDKDG1-----SILDGIPHGTKVTITEKSVPDPYMIDTTPMAATIKAGETI 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           526 A-----TROPIGVEGTMNSQYSDCDPLGNYA-----PYLILRKPGDQTEAAKATM 570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      466 FYLERCDAGAFTGGHGDALKYVTGTFDSEIPCSLCEKHTRPVCAHTTVHRLRQRMPRFGQ 525
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647 TTACNEQLGFDGYGKFENLPYGDYLLEEIFA---PEGFQKITPLEIRSTFKENKDDYAKS 703
                                                                                                                                                                                                                            527 VKGTKASDETVTLALDEKNQVAVKHLAINEYFWQETKAPEGYTLDETKYPVSIKKVDNNE 586
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                                                     806 VDMLHGALGF------PNP 838
                                                                                                                                                                   765 ----VIRDIRVKNRVV-----FSGNCTNLSEAA------RARLVGLASAYQRQEKR 805
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                                                                                                                                                                                                                                                                               ENGGETSTESTTVTLSE-GPVSAPNPTLAQ-----DAPAGETFDGDLARVSVE----- 764
                                                                                                              KNAVITRDVTAKEQVIREGEDEFKEAGSADGTAETGENDLSEKVSPLEGTXEITGAEDKA 646
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18.3%; Pred. No. 0.092;
ative 150, Mismatches 415; Indels 352,
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ction from from ibes genes, is. The prot an infection They can a	Choi GH, Hromockyj A, Kunsch -070095/06. MAX20178. ted Enteroporous faecalls polynum for the detection of Enterococcus	12-NOV-1998. 04-MAY-1998; 98WO-US08959. 14-NOV-1997; 97US-0046609. 16-MAY-1997; 97US-0044631. 16-MAY-1997; 97US-0046655.	Enterococcus faecalis; infection; vaccine; immune response; diagnosis; detection; attenuation; antigenic. Enterococcus faecalis. Wo9850554-A2.	Y00188 Y00188 AAY00188 standard; Protein; 1074 AA. AAY00188; 20-APK-1999 (first entry) Enterococcus faecalis protein EF094.	1103EELHDQ11QTLETFWTVEGALEAVKILDEKTTAGDGETPTNLAFNFD 1149 1		LWTTAFTST	839 QWFWTLLQRNQMPADKLTHEEITTIAAVKRETEEYAAINFINLPPTCIGE 888 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1

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Hest Local similarity 18 0%; prod. No. 0 092;
Matches 206; Conservative 150; Mismatches 415; Indels 352
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99+ AGNNKVFQAGNWSGLNGGKNVCPLFTFDRTRRFIIACFRGGFICFVTGFSSGNRETTLSD 1052
                                                                                                                                           946 AKALLEKTENLPELWITAFIST - - -
                                                                                                                                                                                                               755 LATWKIKINKKLNTLDFTE-LVDKL
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                                                                       TKAAQEKDEKAKPVVIAESTASLANKEKSGTWKILHKUTAEQ+++++-VLDKSIVLENYV-853
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                                                                                                                                                                                                                                                                                                                                                                                                                     -MPADKLTHEEITTIAAVKRFTEEYAAINFINLP--PTCIGE 888
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                                                                                                                                        ---HLVRAAMNQRPMVVLGISISKYHGA 992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides the protein and coding sequences of a number of polypeptides from Enterococcus faecalis. The proteins can be used as vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal, particularly E. taecalis. The polynuclootide is also useful for preventing or treating E. taecalis infection. The present sequence is a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New genes and polypeptides from Enterococcus faccalis, useful as vaccines for preventing, treating or attenuating an infection caused by among the Enterococcus genus in an animal, particularly E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 9; Page 163; 255pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ABN98163
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105 PSMSDKAKLVSVLWEKAGTDIDTNMVAQKMIWEEVNGYKLHSIKRLGGASVDIK-----
                                                                                           310 PSGGFERRLASIM--AADTALHAEVIENTGIYEE-----
                                                                                                                                                                                                                                                                                  250 RVRNVTAVARGAAHLAFDENHEGAVI PPDITYTYFQSSSSGTTTARGARPNDVNSTSKPS 309
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                                                                                                                                                                                                                                                                                                                                                                                             Mismatches 415;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                755 LATWKDGNKKLNTLDETE-LVDKL------RYNLHETKEDWYVVAQATDVEA- 799
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                                                                                             983 -TEINYEKDGNVNGKHNEULKEKSQTLTPKEVPTIPSTPKQPE 1024
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VDMLHGALGF-----PNP 838
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----NIDYRVIGNQLVLTP-------NSNSKSGTLTLKKSAGTGTP-VAYKK 251
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                                                                                                                                                               SCEPSHDTTSNV------LNISGSNISGSTVPGLKRPPEDDE 1185
                                                                                                                                                                                                                              GSKEAFETTLYALLEDGINKETWKSGKTEHEVNUKEFTKTVLAEKVUTGKYFEGTKFTF
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ABP43425 ID ABP XX

ABP43425 standard; Protein; 1074 AA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides the protein and coding sequences of a number of polypeptides from Enterococcus faccalis. The proteins can be used as vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal, particularly E. faecalis. The polynucleotide is also useful for preventing or treating E. faecalis infection. The present sequence is a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Choi GH, Bailey С,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E faecalis EF102 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 9; Page 177; 255pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New genes and polypeptides from Enterococcus faecalis, useful as vaccines for preventing, treating or attenuating an infection caused by a member of the Enterococcus genus in an animal, particularly E.
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359 SMTSKNMRQKGQILLEKTG-VETGTDLWNUNYSLAGNTFAIRKDSPAGEIVQEITTDEKG 417
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mes 206; Conserv
                                          QDTYRATLERLEIDLEGERLIDRGAPGSSEGLS-----SVIVDHPT---FFFILDFLFA 621
                                                                                                                                                                              AGLQTVMAGALDKPNTYAIKINVETKGS-LKIKKIDKESGDIVPETVFHL-----DFGK
                                                                                                                                                                                                                        FYLERCDAGAFTGGHGDALKYVTGTFDSETPCSLCEKHTRPVCAHTTVHRLRQBMPRFGQ 525
                                                                                                                                                                                                                                                                                                               GPSENREYQEAGPHLAANPQTDRDGHVLSSQSTGSSNTEESVDYLALICGEGAPLLARLL 465
                                                                                                                                                                                                                                                                                                                                                            SIEGKINK--AIEEYQKKPSFHNTTVKTILGQSTTLIDKNELNLSEFUKVVQNTA----
                                                                                                                                                                                                                                                                                                                                                                                                      GMEGTLPRLNALGSYTAR------VAGVIG-AMVESPNSALYLTEVEDSGMTEAKDGGP 405
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                                                                                    ALPSKDVTTDKDGI-----SILDGIPHGTKVTITEKSVPDPYMIDTTPMAATIKAGETI 358
                                                                                                                                                                                                                                                                     ----NIDYRVIGNQLVLTP-------NSNSKSGTLTLKKSAGTGTP-VAYKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                PSMSDKAKLVSVLWEKAGTDIDTNMVAQKMIWEEVNGYKLHSIKRLGGASVDIK----- 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSGGFERRLASIM--AADTALHAEVIFNTGIYEE-----TPTDIKEWPMFI 353
                                                                                                                                 A-----PYLILKKPGUQTEAAKATM
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18.3%; Pred. No. 0.092;
ative 150; Mismatches 415; Indels 352; Gaps
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                      23 MAR 2000; 20000S 191637P
11 JUL 2000; 2000US 0614150
                                                                                                                                                            brosophila melanogaster
                                                                  23 MAR 2001; 2001WO US09231
                                                                                                   27 SEP 2001.
                                                                                                                                W0200171042-A2
                                                                                                                                                                                             pharmaceutical.
                                                                                                                                                                                                        Drosophila, developmental biology, cell signalling, insecticide,
                                                                                                                                                                                                                                      brosophila melanogaster polypeptide SEQ ID No 1464.
                                                                                                                                                                                                                                                                        26 MAR 2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          924 GSKEAFETILYALLFOGTNKEIWKSGKIEHEVNDKEFTKTVLAEKVDTGKYPEGTKFTF- 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       876 QAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            587 KNAVITRDYTAKEQVIREGEDEEKFAGSADGTAETGENDLSEKVSPLEGTXEITGAEDKA 646
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                                                                                                                                                                                                                                                                                                                                                                                                                TEINYEKDGNVNGKHNEDLKEKSQTLTPKEVPTIPSTPKQPE 1024
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                                                                                                                                                                                                                                                                                                                                                                                                                                           LNISGSNISGSTVPGLKRPPEDDE 1185
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                                                                                                           FQLAPSKELTYWD-----
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1002 GNWSGLNGGKNVCPLETEDETERFILACPEGGF1CPVTGPSSGNRETTLSDQVRG11VSG 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, SEQ ID NO 1464, 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          841 FWILLQKNQMPALKLIHEEITIIAAVKKETEEY-----AATNETNLPPICI-GELAQ 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     692 FYGQQVEGRN-FRNQFQP----------VLRRRFVDLFN-GGFIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 STSAEFSYVEDIEEREWLARNFETLDQQQ-LCKSERCETAELLIKSQAWDNFMALKFPTV 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           562 QTEAAKATMQD-TYRATLERLEIDLEQERILDEGAPCSSEGL-----SSVIVDHPTF 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         506 PVCAHTTVHRLRQRMPRF-GQATRQPIGVFGTMNSQYSDCDPLGNYAPYLILRKP---GD 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       250 ASEFSEUTEAMSDVISHFHVSEQLKILGKKLSFSMVKN----PSHLEAANPVAMGKTRS- 304
                                                                                                                                                                                                                                                                                                                                                                                            FYMA-NLILKYCDHSQYLINTLTSIITGAPPPPDPSSVLHWI-RKDVTSAAD------I 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DD--PEALARVTSLAFRYQR-EFRKDI-----FIDLNCFRRIVHQRESVPD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KRYGGEGAESMLAFFWQLLRDSVQAN1EHVVLAMPHRGRTPLQAALLNMRPAKVFRKLSG
                                                                                            KTHVNARLKKLENGVKIDWSTA------EALAIGSLMYQG--HNVRI---
                                                                                                                                                                                              ETQAKALLEKTENLPEL-WTTAFTSTHLVRAAMNQRPMVVLGISISKYHGAAGNNKVFQA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----IVNNQVGFTTPGDRGRSTAYTSDLAK-S1QA------PVFHVNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RSITVTLSEGPVSAPNPTLGQDAPAGR----TFDGDLARVSVEVIRDIRVKNRVVFSGNC 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PISIRTSQQELQELSPAFYGLQTQEPVRTEGLL----SGPQVAHNVAQLEQLLKDIYCGR 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----LYAQQLAKEQVLSESKAKEMRDEYMKYLGEELALAPAYQPPPSYFEKOWTN 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TNLSEAARARLVGLASAYQRQEKRVDMLHGALGFL-LKQFHGLLFPRGMPPNSKSPNPOW 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --KOQARGEGAFGDGSQPFGEHVI.NVILHGDAAFAGQGINQECI.NMAYVPHFEVGGSI.HI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RR-----TQFMKVLVETRDYKI----REG 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative 88; Mismatches 266; Indels 257; Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.9%; Score 122.5; DE 20.2%; Pred. No. 0.076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Li PWD,
                                                                                                                                                                                                                                                                                               ----TGL-----DYSLLHYTGQQSVTFPEDFNIRPHLL 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----AFCPTTNFLVKRTHLAVVQDLALSQCHCV 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Myers EW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           St
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
          cc upregulated by about 3 fold in cells subjected to mechanical strain.

CC The specification describes a method for the identification of genes

CC responsive to a specific mechanical stress. The method comprises applying

CC the mechanical stress to an organism (tissue or cells comprising bone

CC colis), isolating the specific cellular fractions and extracting mRNA

CC from them, and differentially analysing the mRNA in comparison with

CC control samples. The method is used to identified genes whose expression

CC is responsive to a specific stress. The identified genes are employed in

CC determining risk associated with a physiological or disease state. The

CC invention, are used for treating a medicament for gene

CC invention, are used for treating or controlling a

CC physiological or disease state (especially osteoporosis or bone density

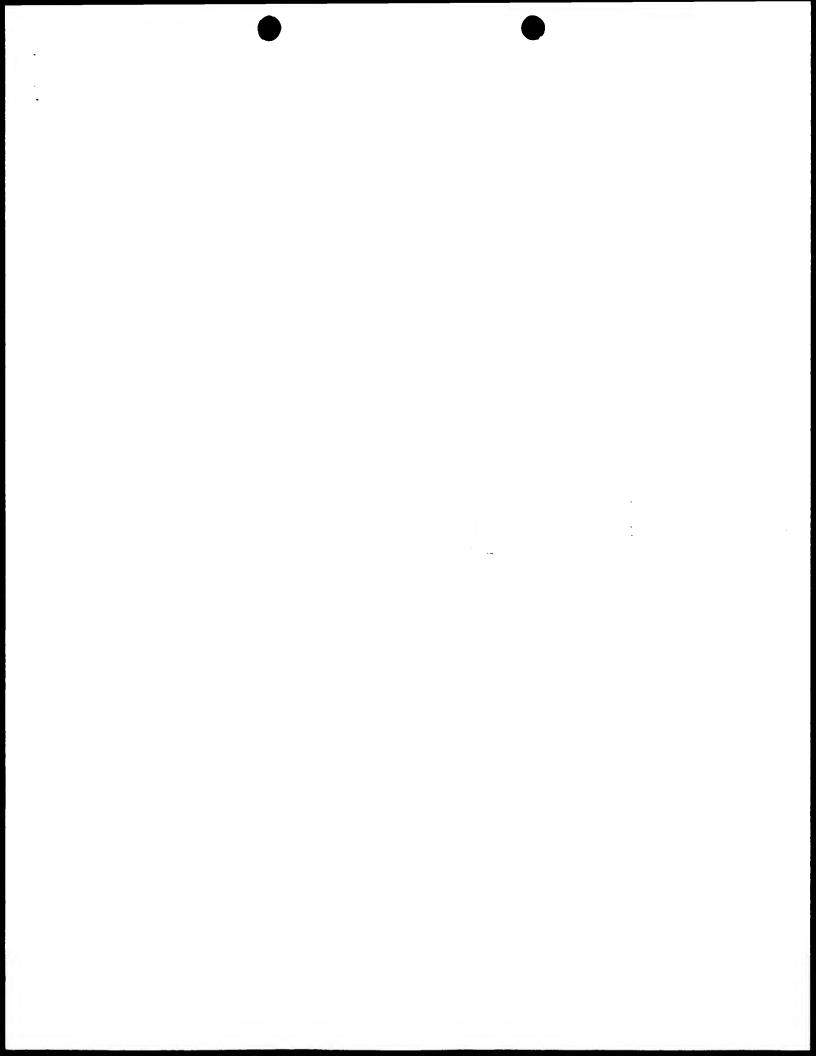
CC or other factors causing or contributing to osteoporosis or its symptoms

CC methods can also be used for advancing research or studies in bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note* "encoded by GGA" Misc-difference 1453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY53665 standard; Protein; 2387 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1116 PWTVEGAL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9960164-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mechanical stress induced protein 608 amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY53665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1062 GAMVQLAIYATVVRAVGAKAQHMAFDD-----WLSLTDDEFLARDLEELHDQIIQTLEI 1115
                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents protein 608, which was identified using the method of the invention after subjecting rat osteoblasts to mechanical stress. Expression of the 608 gene was found to be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 32, Fig 5A·Z, 308pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identification of stress induced genes for determining risk and preventing, treating or controlling osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAZ36322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI: 2000-054404/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Einat P, Mor O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (QUAR-) QUARK BIOTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-NOV-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bone development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mechanical stress; gene therapy; protein 608; osteoporosis; bone density;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            669 KWMESNALVMLLPHGYDGAASEHSSCRIERFLQLCDSKETSADGDS 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  611 GGKLELAHSILSEEAVLGFEYGMAIDNPNNLIIWEAQFGD··FANGAQIIIDTFIVSGET 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9805-0085673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US11066.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "encoded by NTT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "encoded by CAT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Skaliter R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------BAVKILDEKITAGDGET 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Feinstein E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Faerman A;
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756	703 AHPVTGUN MATYGHTNTYSSETSKASTVLQPINFTESYGFQIFTTGVSRPSSSD 7	ф		
1045	1007LNGGKNVCPLFTFDRTFRFIIACPRGGFICPVTGPSSGN 1	Оу		
702	IFP-SVA	dd		
1 aus	961 TTAFTSTHLVRAAM	νý		
649	593 DEEFMYLKTKASGVPGKSPTADSGPVNHGFMTSlASGTEVSTVNPQTLQ-SEHLPDFK	DЬ		
960	901 YCDHSQYLINTIJISLITGARKEKDESSVLHWIRKDETSAADIETQAKALLEKTENLEELW	Qy		
592	556 NSVPKKQENTTVKPVPLAVPLVELTDEEKDASGMI - PP	Бþ	-	
900	848 NOMPADKLTHEEITTIAAVKRFTEEYAAINFINLPPTCIGELAQFYMANLILK	Qy		
555	502VSGVHRKNKHRDLIHRRRGDSTLRRFREHRRQLPLSARRIDPQRWAALLEKAKK	Db		
847	792 LVGLASAYUKÇEKRVDMLHGALG-FILLKQFHGLLEFRGMPPNSKSFNPQWFWTLLQR	7,4		
501	448 FKVSVQKKGQRMVEHDREAGGSGLGE-PNSSVSLKQPASLKLSASALTGSEAGKQ-	Dh		
791	744	Qy		
447	399 LPGNTVESQPSRDRQILNNGTLRILQVT-PKDQGHYQCVAANPSGADESS	Db		
743	692 FYGQQVEGRNERNQFQPVLRRREVDLENGGEISTRSITVTLSEGPVSAPNPT	Qy		
398	352 LTYRITVVEPYCESTHDSGVOHTVVTGETLDLPCLSTGVPDASISWI	Db		
691	REGLS	Qy		
351	292 DPSPHLEWLLADGSKVPAPYVSEDGPILIDKNGKLELQMADSFDAGLYHCISTNDADADADV	Db		
639	602LSSVIVDHPTFRRILDTLRARIE-QTTTQFMKVLVETRD	QУ		
291	232 ATTLSTLQIQESTDAQIALPRAEMRAERLKWTMICMMNNPKLEPTVLVGGTIALSCPGKG	Дb		
601	562 QTEAAKATMODTYRATLERLEIDLEQERLLDKGAPOSSEG	Qy		
231	173 DSPLILERKPOLIETESLSSKYKÖVALRPEDIFTSIEAUVK-ADPEWFÖGEKIVÄGLRRT	dc		
561	512 TVHRLRQRMPKFGQATRQPIGVFGTMNSQYSDCDPLGNYAPYLILRKPGD	Qу		
172	124 IQKPSRTSPTAFTEENDYIMLNASFSTNLVCSVDYNHIQPVWQLLALYS	рb		
511	456 FGAPLLARILIFYLERCDAGAFTGGHGDALKYYTGTFDSE1PCSLCEKHTRPVCAHT	Qy		
123	64 SGAFLCTKPTIDPSLKSKSLVTQEDNGSASTSPQDFIEPFGSLSLNMTDLSGNKADMVCS	Db		
455	416 AGPHLAANPQTDRDGHVLSSQSTGSSNTEFSVDYLALICG	Qу		
Gaps 40	Query Match 1.9%; Score 122.5, DB 21; Length 2387, Best Local Similarity 18.6%; Pred. No. 0.42; Matches 145; Conservative 114; Mismatches 286, Indels 233; Ga	Md Be		
	Sequence 2387 AA;	SQ		
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Search completed. March 28, 2003, 13:35.35

Jub time : 96 secs



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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Result
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 btal number of hits satisfying chosen parameters:
                                                                                                              pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1: /cgn2_6/pindata/1

2: /cgn2_6/ptodata/1

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4: /cgn2_6/ptodata/1

5: /cgn2_6/ptodata/1

6: /cgn2_b/ptodata/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
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6294
1 MENTQKTVTVPTGPLGYYYA......DELFDLSGIPIKHGNITMEM 1203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           262574 seqs, 29422922 residues
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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                                                             SUMMARIES
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1141.799 Million cell updates/sec
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No.	Score	Match	Length	DВ	ID	Description
1	3054	48.5	1452	4	US-09-127-227-2	Sequence 2, Appli
2	183	2.9	35	N	US-08-807-332B-9	9,
ω	183	2.9	35	4	-09-338-	`
4	131		757	4	-413-814-	4
υī	123	2.0	1074	4	us-09-071-035-358	,
6	123	2.0	1074	4	US-09-071-035-394	Sequence 394, App
7	111	1.8	5215	4	us-vy-1v5-537-2	2, A
8	106.5	1.7	3567	^	US-U7-642-734C-4	Sequence 4, Appli
9	106.5	1.7	3567	w	US-08-439-009A-4	Sequence 4, Appli
10	106	1 7	774	_	US-07-731-157A-7	Sequence 7, Appli
11	106	1.7	774	2	US-08-541-780-7	Sequence 7, Appli
12	105	1.7	774	۔۔	US-08-633-760-46	Sequence 46, Appl
13	105	1.7	774	_	US-08-633-760-48	Sequence 48, Appl
14	104.5	1.7	635	4	US-08-931-608A-5	Sequence 5, Appli
15		1.7	774	-	US-08-019-870-5	Sequence 5, Appli
16	103	1.6	774	_	US-08-019-870-3	Sequence 3, Appli
17	103	1.6	774		US-Ü8-633-760-44	Sequence 44, Appl
18	102	1.6	729	_	US-08-070-165F-6	Sequence 6, Appli
19	102	1.6	724	t.	US-08-885-418-6	Sequence 6, Appli
120	701	<u>⊢</u>	774	←	ns-07-747-901A-3	Sequence 3, Appli
21	102	1.6	774	_	пs-07-935-312-3	Sequence 3, Appli
13	102	1.6	774	_	US-08-633-760-50	Sequence 50, Appl
23	101.5	1.6	773	_	US-08-019-870-1	Sequence 1, Appli
24	101.5	1.6	773		US-08-019-870-6	Sequence 6, Appli
25	101.5	1.6	774		US-08-019-870-8	Sequence 8, Appli
25	101.5	بر 1	774	_	ns-08-019-870-11	11,
27	101.5	1.6	774	Н	US-08-633-760-52	Sequence 52, Appl

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	63	t.
97.5	97.5	98	98	98.5	98.5	99	100.5	100.5	100.5	101	101	101	101	101	101	101	TOT
1.5	1.5	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	
1024	769	821	821	2152	2152	915	2616	1321	1321	7257	7257	7257	7257	7257	7257	7257	104.4
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US-09-562-737-50	US-08-471-570-8	US-08-323-430-13	US-08-451-822A-13	US-09-370-700-3	US-09-036-987A-3	US-08-328-322-5	5206163-3	PCT-US95-07744A-3	US-08-261-822A-3	US-09-567-899-5	US-09-568-472-5	US-09-568-486-5	US-09-568-480-5	US-09-567-969-5	US-09-568-102-5	US-09-335-409-5	かん カー・スイト・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・
Sequence	Sequence	Sequence	Sequence	Sequence 3,	Sequence 3,	Sequence 5, Appl	Patent No. 520616	Sequence	Sequence	Sequence 5,	Sequence 5,	Sequence	Sequence	Sequence	Sequence	Sequence	
50, App.	e 8, Appli	13, App.	13, App1			5, Appli	5206163	3, Appli	3, Appli		5, Appli	5, Appli		5, Appli	5, Appli	5, Appli	

ALIGNMENTS

Qy	Qy Db	Оy	Db	Qу Db	Qy Db	Qу	Que Bes Mai	US-00	RESUL US-09 ; Seq ; Pat ; Pat ; GEN	
Qy 356 EGTLPRLNALGSYTARVAGVIGAMVESPNSALYLTEVEDSGMTEAKDGGPGPSFNRFYQF	QY 296 GARRNDVNSTSKPSPSGGFERPLASIMAADTALHAEVIENTGIYEETPTDIKEWPWFIGM	Qy 236 LIHDCVIAPMAVALEVRNVTAVARGAAHLAFDENHEGAVLPPDITYTYFQSSSSGTTTAK 	QY 176 GGLDIVHINHGDVIRIPLEPVQLEMPDVNRLVPDPFNTHHKSIGEGEVYFTPFYNTGLCH 235	QY 116 ARERFGFSRCQGPPVDGAVETTGAEICTRLGLEPFNTILYLVVTALFKEAVFMCNVFLHY	Qy 56 KTFTSSLAVVSGARTTGLAGAGITLKLTTSHFYPSVFVFHCGKHVLPSSAAPNLTPACNA ::: : ::	Qy 1 MENTOKTVTVPTGPLGYVYACRVEDLDLEEISFLAARSTDSDLALLPLMRNLTVE	Query Match 48.5%; Score 3054; DH 4; Length Best Local Similarity 49.8%; Pred. No. 1.8e-304; Matches 609; Conservative 200; Mismatches 36b; Indels	TITLE OF IN TITLE OF IN TITLE OF IN FILE REFEREN CURRENT APP. CURRENT FIL. NUMBER OF SI SOFTWARE: F SOFTWARE: F SOFTWARE: P TYPE: PRT ORGANISM: S-09-127-227-	RESULT 1 US-09-127-227-2 US-09-127-227 Sequence 2, Application US/09127227 Patent No. 6399354 GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: David M. Knipe APPLICANT: Travis J. Taylor APPLICANT: Travis J. Taylor	
TEAKDGGPGPSFNRFYQF 415	VEUREBEUDIKEMBMETCM 355 THE HE HE I VEUREBEUDIKEMBMETCM 351	DITYTYPQSSSSGTTTAR 295 - :: 	IGEGEVYPTPFYNTGLCH 235 	TEALEKEAVEMONVELHY 175 	HYLPSSAAPNLTPACNA 115 	STDSDLALLPLMRNLIVE 55	Length 1452; Indels 48; Gaps 17	pressing A		

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                                                                                                                                                                                                                                                                                          Sequence 9. Application US/08807332B
Patent No. 5959074
                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                              APPLICANT: Dreyins, bavid H.
APPLICANT: Geliand, Erwin W.
FITLE OF INVENTION: PRODUCTS AND PROCESSES FOR REGULATION OF
                                                               CORRESPONDENCE ADDRESS:
                                                                                                NUMBER OF SEQUENCES:
                                                                                                                              TITLE OF INVENTION:
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      STREET:
                                       ADDRESSEE
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1700 Lincoln St., Suite 3500
                                    Sheridan Ross
                                                                                                                              GENE RECOMBINATION
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RESULT 3
US-09-338-876-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No.
GENERAL II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/09338876
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TELEFAX: 303/863-0223
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
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               REFERENCE/DOCKET NUMBER: 28 TELECOMMUNICATION INFORMATION:
                                                                                     FILING DATE: 28-FEB-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Dreyfus, David H.
APPLICANT: Geliand, Erwin W.
TITLE OF INVENTION: PRODUCTS AND PROCESSES FOR REGULATION OF
TITLE OF INVENTION: GENE RECOMBINATION
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APPLICANT:
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TELECOMMUNICATION 1NFORMATION:
TELEPHONE: 303/863-9700
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ATTORNEY/AGENT INFORMATION:
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 TELEPHONE:
                                                     REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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                                                                      NAME:
                                                                                                                                                                                                APPLICATION NUMBER: US/09/338,876
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OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 84. Application US/09413814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Sorangium cellulosum
-09-413-814-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide TITLE OF INVENTION: heteropolyketide compounds FILE REPERENCE: PCT/US 99/23535 CURRENT APPLICATION NUMBER: US/09/413.814 CURRENT FILING DATE: 1999:10:007 EARLIER APPLICATION NUMBER: DE 198 46 493.2 FARLIER FILING DATE: 1998:10:09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Mueller, Joachim APPLICANT: Reichenbach, Hans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hofle, Gerhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Goldberg, Steven L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Dougherty, Brian A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cino, Paul M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Brandt,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bloecker,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Beyer, Stefan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bristol-Myers Squibb, Co.
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305 VRKSSEEFRAALD------IRSWEVAFTGAEPVRADTLDRFARAFAVSGERRE--AFYP 355
                                                                                                                                                                                                                                                                                                                                       110 TRACNAAREREGESROOGPPVDGAVETTGAEICTRLGLEPENTILYLVVTALFKEAVFMC 169
                                                                                                                                           225 PTPFYNTGLC-----HLIHDCVTAPMAVALF---VRNVTAV---AKGAAHLAFD-- 267
                                                                                                                                                                                                                                                                                                                                                                                                                                  54 VEKTETSSLAVVSGART - - - TGLAGAGITLKLTTSHEYPSVEVEHGGKHVLPSSAAPNI. 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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                                             ----ENHEGAVLPPDITYTYFQSSSSGTTTARGARRNDVNSTSKPSPSGGFEKKLASIMA 323
                                                                                           LPPYHDMGLIGGILQALYRRIRVALMSPLSFLQRPMRWLRAVSALGASVSGGPNFAYDLC
                                                                                                                                                                                           ·AFLQYTSGSTGEPKGVMLTHGNL····LHNSRLIAHGFDLTSPDPV------GVIW 244
                                                                                                                                                                                                                                         NVFLHY - - - - GGLDIVHINHGDVIR1PLEPVQLEMPDVNRLVPDPFNTHHRSIGEGEVV 224
                                                                                                                                                                                                                                                                                                                                                                                     LERTLPRVASIVADARAEAALTSSAVAGIVAS-------LPASAAA-- 167
                                                                                                                                                                                                                                                                                         35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.1%; Score 131; DB 4; Length 757;
21.1%; Pred No. 0.00079;
ative 84; Mismatches 251, Indels 212, Gaps
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; TOPOLOGY: linear ; MOLECULE TYPE: protein 
HS-09-071-035-358
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                                                                                                                                                             TELEFAX: (301) 309-8512 INFORMATION FOR SPQ ID NO:
                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: PH
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides NUMBER OF SEQUENCES: 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                547 IVAAREAVTAEHO----LVAHAVALIAPGALPKTSSGKVRRRECRRAFLE----DALGER 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            491 -----FDSE1PCSLCEKH--TRPVC--AHTTVHRLRQRM------PRFGQATRQ 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            433 LSSQSTGSSNTEESVDYLALICGFGAPILLARLIFYLEFCDAGAFTGGHGDALKYVTGT-- 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        404 SGKALDPKA---VALVDPAG----NELGPG-EIGELW-VSGPSVAVGYWGRPE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   652 PISRFGLDSLAAVELQHAFQVRTGRAIPLTSIL 684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS VE
SOFTWARE: ASCII Text
                                                               TYPE: amino acid
STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                              NAME:
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                                                                  single
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Best Local Similarity 18 0%; Prod No. 0.01;
   103
                                                                                                                      105 COVRCTIVEGGAMVQLATYATVVRAVGAR------AQHMAFDDWLSLTDDEFLARDL-- 1102
                                                           876 QAQ
                                                                                                                                                                                           854 YENKVAFEAGNE-
                                                                                                                                                                                                                                                                                                              800 TKAAQEKDEKAKPYVIAETTATLANKEKTGTWKILHKLTAEQ------VLDKSIVLENYV 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        527 VKJIKASDLIVILALDEKNQVAVKHLAINEYEWQEIKAPEGYILDEIKYPVSIKKVDNNE 586
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EELHIQTTOTLETPWIVEGALEAVKILDE -
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---KITAGD----GETPINLAFNED 1149
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; Patent No. 6448043
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                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.0%; Score 123; DB 4; Length 1074; Best Local Similarity 18.3%; Pred. No 0.01; Matches 206; Conservative 150; Mismatches 415; Indels 352; Caps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (301) 309-851
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1150 SCEPSHDTTSNV------LNISGSNISGSTVPGLKRPPEDDE 1185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                  466 FYLERCDAGAFTGGHGDALKYVTGTFDSELPCSLCEKHTEPVCAHTTVHRLEQRMPRECO 525
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                                                               212 ----NIDYRVIGNQLVLTP-------NSNSKSGTLTLKKSAGTGTP:VAYKK 251
                                                                                                          406 GPSENRFYQEAGPHI.AANPQTDRDGHVLSSQSTGSSNTEFSVDYLAI.ICGFGAPI.I.ARI.L 465
                                                                                                                                                                                                    354 GMEGTLPRLNALGSYTAR-----VAGVIG-AMVFSPNSALYLTEVEDSGMTEAKDGGP 405
                                                                                                                                                                                                                                                105 PSMSDKAKLVSVLWEKAGTDIDTNMVAQKMIWEEVNGYKLHSIKRLGGASVDIK----- 158
                                                                                                                                                                                                                                                                                           310 PSGGFERRLASIM -- AADTALHAEVIENTGIYEE --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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                                                                                                                                                                                                                                                         Sequence 2. Application US/09105537A Patcnt No. 6265202 GIMERAL INFORMATION. APPLICANT: Sherman, D.H.
TITLE OF INVENTION: DNA encoding methymycin and pikromycin FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/105,537A
CURPENT FILING DATE: 1998-06-26
NUMBER OF SEV ID NOS: 43
                                                                                                                                                              APPLICANT: Liu, H. APPLICANT: Xue, Y. APPLICANT: Zhao, L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       839 QWFWTLLQRNQ------MPADKLTHEEITTIAAVKRFTEEYAAINFINLP--PTCIGE 888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 A 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   676 HLAVVQDLAL------SQCHCVFYGQQV-----EGRNFRNQFQPVLRRRFVDL 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   418 RAE--TPKELANALELGTYYVTE--TKSSNGFVNTFKPTKVELKYANQTVALVTSNVKGQ 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    647 TTACNEOLGFDGYGKFENLPYGDYLLEELEA----PEGFQKITPLEIRSTFKENKDDYAKS 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                806 VDMLHGALGF------PNP 838
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                359 SMTSKNMKQKGQILLEKTG-VETGTDLWNDNYSLAGNTFAIRKDSPAGEIVQEITTDEKG 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         526 A----TRQPIGVFGTMNSQYSDCDPLGNYA-----PYLILRKPGDQTEAAKATM 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  924 GSKEAFETILYALLPDGINKEIWKSGKIEHEVNDKEFIKTVLAEKVDIGKYPEGIKEIF- 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               876 QAQ-----TVNCTIERHVSIQTKAHLEDGSQTFTHGDVMDMFDDVSVTHDVLD 923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               854 YENKVAFEAGNE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     800 TKAAQEKUEKAKPYVIAETTATLANKEKTGTWKILHKLTAEQ------VLUKSIVLENYV 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 946 AKALI.EKTENLPELWTTAFTST------HLVRAAMNQRPMVVI.GISISKYHGA 992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              889 LAQFYMANLILKYCDHSQYLINTLTS11TGARRPRDPSSVLHWIRKD---VTSAAD1ETQ 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          704 EYVFTITEEGQKQPIKMYTVPYEKLTNNE-----FSVSLNRLMLYDLPEKEDSLTS 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          718 FNGGFISTKSITVTLSE-GPVSAPNPTLGQ------DAPAGRTFDGDLARVSVE----- 764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         252 AGLQTVMAGALDKPNTYAIKINVETKGS-LKIKKIDKESGDIVPETVFHL-----DFGK 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            983 -TELNYEKDGNVNGKHNEDLKEKSQTLTPKEVPTIPSTPKQPE 1024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VKGTKASDETVTLALDEKNQVAVKHLAINEYFWQETKAPEGYTLDETKYPVSIKKVDNNE 586
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LATWKDGNKKLNTLDFTE-LVDKL-------RYNLHEIKEDWYVVAQAIDVEA- 799
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; TYPE: PRT; ORGANISM: Streptomyces venezuelae US-09-105-537-2
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SEQ ID NO 2
LENGTH: 5215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           439 EETPV------DSGAALPFVVTGRGGEALRAQARRLHEAVEADPELAP 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               403 GGPGPSFNRFYQFAGPHLAANPQTDRD------GHVLSSQSTGSSNTEFSVD 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163 KEAVFMCNVFLHYGGLDIVHINHGDVIRIPLFPVQLFMPDVNRLVPDPFNTHHRSIGEGF 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103 SSAAPNLTRACNAARERFGESRCQGPPVDGAVETTGAEICTRLGLEPENTILYLVVTALF 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166 SLTVDAAQSSSLVAVHLACESLRAGESTTALV-AGVNL------NILA 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                481 AALARSLVTTRTVFTHRSVVLAPDRARLLDGLGALAAGTPAPGVVTGT------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       304 YVELHGTGT-------PVGDPIEAAALGAVLGSARPADEPL------LVGSA 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   283 YFQSSSSGTTTARGARRNDVNSTSKPSPSGGFERRLASIMAADTALHAEVIFNTGIYEET 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  262 IRASAVNNDG-----
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867 KRFTEEYAAINFINLPP--TOIGELAQFYMANLILKYCDHSQYLINTLTSIITGAPPPPD 924
                                                                                                                                                                                                                                                                                                                                                                                                                                                 616 PDLLAGH----SVGEISAAHVAGV--LSLRDA-----ARLVAARGRLMQALP----- 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          657 FDPYSGAFCPITNFLVKFTHLAVVQDLALSQCHCVFYGLQVEGRNFRNQFQPVLPPRFVD 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             556 HPAFATAFDAVAAELDPLLDRPLAELVAAGDTLDRTVHTQPALFAVEVALHRLVESWGVT 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  609 HPTFRRILDTLRARIEQTTTQFMKVLVETRD------YKIREGLSEATHSMALI 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 549 NYAPYLILRKPGDOTEAAKATMQDTYRATLERLFIDLEQERLLDRGAPCSSEGLSSVIVD 608
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                                                               742 EELDFQEPRVDVVSTVTGLPVTA----GQWTDPEYW-----VDQV-RRPVRFLDAV 787
                                                                                                                                                                                          695 LAG-----AERAVLDVAELLREQGRRTKRLSVSHA------FHSPLMEPMLDDFRRVV 741
                                                                                                                                                                                                                                                          717 LFNGGFISTRSITVTLSEGPVSAPNPTLGQDAPAGRTFDGDLARVSVEVIRDIRVKNRVV 776
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----SRALADGDRVH-----CV 261
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                                                                                                                                                                                                                                                                                                                      --EGGAM----VAVEASEEEVL---PHL----AGRERELSLAAVN-----GPRAVV 694
                                                                                                                              ----PR-----GMPPNSKSPNPQW----FWTLLQRNQMPADKLTHEEITTIAAV 866
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US 07 642 7340 4
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  Query Match 1.7%; Score 106.5; DB 2; Hest Local Similarity 19.9%; Pred. No. 4.8; Matches 287; Conservative 104; Mismatches 384;
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Patent No. 5824513
                                                                                                MOLECULE TYPE: protein
07 642 7340 4
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APPLICANT: Katz, L
APPLICANT: Mealpine, J
APPLICANT: Mealpine, J
FITLE OF INVENTION: Recombinant DNA Method for Producing
FITLE OF INVENTION: Erythromycin Analogs
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3567 amino acids
                                                                                                                   Type: amino acids
Type: amino acids
Type: amino acid
TypeOLOGY: line:
                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          AUTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPERATION SYSTEM: PLOSZMS DOS
SUFTMARE: Putentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1082 QHMAFDDWLS - LTDDEFLARDLEELHDQIIQTLETPWTVEGALEAVKILDEKTTA 1135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          906 VTSGEGEGEGEGAGAGGGDRPARHETT -- ERVRAHVAA------ VLEYDDPTRVELGLTF 957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        875 ERHWEDGAARTAAFLTAGR SGTGAG -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   844 POSILIMALITYFYRGHDYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Edward H. Gorman
STREET: Abbott Laboratories D377/AP6D-2 One Abbott
STREET: Park Rd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    985 SISKYHGAAGNNRVFQAGNWSGLNGGKNVCPLFTFDRTRRFIIACPRGGFICPVTGPSSG 1044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /BB RTLEESCADTFLELGPDGVCSAMAADSV-----RDQEAATAVSALRKG--RP-E 833
                                                                                                                                                                                                                                                                  TELEPHONE: 708-937-9396
TELEFAX: 708-938-2623
                                                                                                                                                                                                                                                                                                                                     REFERENCE/IXXIKET NUMBER: 4952.US.01
                                                                                                                                                                                                                                                                                                                                                              NAME: Danckers, Andreas M
REGISTRATION NUMBER: 32651
                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Abbott Park
STATE: 1L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRY: US
60064 3500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 JAN 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US/07/642,734C
                                                                                                                                                                                                                                                                                                                                                           32652
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                                                   DB 2; Length 3567;
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       Indels 465;
Gaps
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2005		1979	Db
1037	GGKNVCPLETEDPTPREIIAGPRGGEIGP	978	Qy
φ.	LPFVLSGRSEAVVAAQARALAEHLROTPELGLTDAAWTLATGRAREDVKAAV	1926	υb
477	VLHWTRKDVTSAADTETOAKALLEKTENLDELWTTAFTESTHL-VRAAMNOR	925	Ογ
1925		1888	da Ga
<u>ې</u>	TREBURATION I POTE TOUR TOURNAMENT TO ANALYSIS TO TOUR TOURNESS TO THE TREE TOURNESS TO THE TREE TOURNESS TOURNESS TO THE TREE TOURNESS TO	90 57	0
864 1887	adagelenger er geben er ge	1837	Db 4
` '		611	
96.81 01.8	SYPVIRDIRVKNRVVFSGNCTNLSEAARARLIVGLASAYQRQEKRVDMLHVSYPVIRDIRVKNRVVFSGNCTNLSEAARARLIVGLASAYQRQEKR	761 1783	0 0 0
1782	Ĝ	17.32	r Dn
760	ĞFĞPVI.KKKEVDI.FNGGFTSTKSTTVTL.SEĞPVSAPNIPT.GQDAPAĞKTETGDI.AR 	705	Ŷ
1731	ACCOVITYMSDPYTFVDFSTQRGLA-SDGRCKAFSARADCFALSEGVAAL	1685	Пр
704	TFDPYSGAFCPITNFLVKRTHLAVVQDLALSQCHCVFYGQQVEGRNFFN	656	Qy
1684	VDGYOGLGNSASVLSGRIAYTEGWEGPALTVDTACSSSLVG1HLAMOALRRGECSLAL	1627	Db
655	DYKIREGISEATHSMAL	615	Qy
1626	ITPREALAMDPOORLMLETAWEAVERAGIDPDALRGTDTGVFVGMNGQSYMOLLAGEAER	1567	DЪ
614	KATMODTYRATLERLFIDLEQERLLDRGAPCSSEGLSSVIVDHPTFRR	567	Oy
1566	PEQLMRVLAEGANI.TTGEPADRGWD.I.GH.; HPDPDNPGTSYVDXGGFI.TDAADFDPGFFG	1507	սե
566	YLILR	552	Qy
1506	VFDHPTVTALAQHL.RARLVGDADQAAVRVVGAADESEPIAIVGIGCREPGGIGS	1453	υb
155	SÝYSDCDPLAYODORYÝS	505	γQ
1452	RAFSELGLDSLNAMALRKRLSASTGLRLPASL	1421	Db
504	LFYLERCDAGAFTGGHGDALKYVTGTFDSE1PCSLCEKHT	445	Qy
1420	GGQAEAEEDS-GFTGEPAQRIAGUSPDEQOENLLELVANAVAEVI.GHESAAEINVR	1366	Db
444	SGMTEAKDGGFGFSFNRFYQFAG	395	Qу
1365	AGPVSVAVADV-DWPVLSEGFAATRPTALFAFI.AGR	1331	Пр
394	TGTYEETPTDIKEWPMFI-GMEGTLPRINALGSYTARVAGVIGAMVESPNSALYLTEVED	336	Qy
130	ARGRSCTSVAMTPWALPGGAVDDGYLRERGLRS-LSADRAMRTWERVLA	1283	DЪ
335	YFQSSSSGTTTARGARRNDVNSTSKPSPSGGFERRLASI	283	Qy
1282	AVI-DEVIGORAVEREVVOSSVAGIWGGAGMAAVAAGSAVIDALAEHHR	1235	Dφ
282	HLIHDCVIAPMAVALRV	235	Qy
1234	ACTL TNPGSISEVAPEEF	1206	i Dp
2 34		175	Qy
1205	: : -: AVVCAQDAAALREA:	1165	Db
774	COGDPVIDGAVETTGAE I OTR I GLEDENTT - YLVVTTATEXEAVEMONVET H	125	0ν

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, Sequence 4, Application US/U8439ົນປຶ່ງA
, Patent No. 6004787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-439-009A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Dundin, s
APPLICANT: Katz, L
APPLICANT: Mcalpine, J B
TITLE OF INVENTION: Method of Directing Biosynthesis of
TITLE OF INVENTION: Specific Folyketides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CPERATINS SYSTEM: PC-D-05/MS-D-05
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1038 VTGPSSGNRETTLSINGVRGTIVSGGAMVQLATYATVVKAVGARAQHMAFDDWLSLTDDEF 1097
                                                                                                                                                                                                                                                                                                          1165 CPGDDLLAAVEEAGASAVVCAQDAAALREALGDEP------VTAL------VH 1205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE. protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 3567 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 49
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2027 MARDLLESSEVFAESMSRCAEALSPHTDW------KLLD--VVRGDG 2065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1098 LARDLEELHUQIIQTL-----ETPWTVEGALEAVKILDEKTTAGDG 1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2006 VT---SAPRKPVL----
                                              1283 ----ARGRSCTSVAWTPWALPGGAVDDGYLRERGLRS-LSADRAMRTWERVI.A 1330
                                                                                                                                 1235 AVL-DEVLGDRAVEREVYCSSVAGIWGGAGMAAYAAGSAYLDALAEHHR------ 1282
                                                                                                                                                                                                                      1206 AGTL----TNFG------SISEVAPEEF------AETIAAKTALL 1234
                                                                                                                                                                                                                                                                                                                                                     125 CQGPPVDGAVETTGAE--ICTR-----LGLEPENTILYLVVTALFKEAVFMCNVFLH 174
                                                                                                                                                        175 YGGLDIVHINHGDVIRIPLEFVQLEMPDVNRLVPDPENTHHKSIGEGEVYPTPEYNTGLC 234
336 TGIYEETPTDIKEWPMFI-GMEGTLPKLNALGSYTARVAGVIGAMVFSPNSALYLTEVED 394
                                                                                     283 YFUSSSSGTTIAKGAKRNDVNSTSKPSPSG----GF--ERRLASIMAADTALHA-EVIFN 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: Abbott Lah
STREET: Park Rd
CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Casuto, Dianne REGISTRATION NUMBER: 40,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/439,009A FILING DATE: 11-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
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N: 435
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SMSRCAEALSPHTDWKLLDVVPGDG 2065	7 MARDILESSEVFAESMSRCAEALSPHTDW	2027	Db	
TLETPWTVEGALEAVKILDEKTFAGDG 1138	LARDLEELHDQIIQTL	1098	QY	
	VTSAPRKPVL	2006	Db	
VTGPSSGNKETTLSDQVRGIIVSGGAMVQLAIYATVVRAVGAKAQHMAFDDWLSLTDDEF 1097		1038	Qy	
-LGDDRAGVCAELDALAEGK		1979	, pb	,
ISISKYHGAAGNURVEQAGNWSGLNGGKNVCPLFTFDRTKRFIIACPROGFICP 1037	PMVVLG	978	į Qy	
AAQARALAEHLRDTPELGLTDAAWTLATGRAFFDVRAAV 1978	PLPFVLSGRSEAVVAA	1926	Дb	
AADIETQAKALLEKTENLPELWTTAFTSTHL-VRAAMNOR 977	5 PSSVLHWIRKDVTSAADIE	92	Qy	
FGVSGTNAHVIVEEAPAEQEAARTERG 1925	GERPRRAGVSSFGVSGT	1888	Db	
AVKRETEEYAAINFINLPPTCIGELAQFYMANLILKYCDHSQYLINTLTSIITGARRPRD 924		865	Qy	
MRHGML-PRSLHADELSPHIDWESGAVEVLREEVPWPA 1887	AAAGAAGVIKVVLAMRI	1837	Db	
GALGELLKQFHGLLFPRGMPPNSKSPNPQWFWTLLQRNQMPADKLTHEEITTIA 864	!	811	Qy	
VEAHGTGTELGDPIEAGALIATYGQDRDRPLRLGSVKTNIGHTQ 1836	3 SGVPA-ADVDVVEAHGTGTELGDPIEAG	1783	Дb	
VSVEVIRDIRVKNRVVFSGNCTNLSEAARARLVGLASAYQRQEKRVDMLH 810		761	Qy	
NGHQVLAVLRGSAVNQDGASNGLAAPNGPSQERVIRQALAA 1782	VLEPLSRARANG	1732	Дb	
QFQPVLRRRFVDLFNGGFISTRSITVTLSEGFVSAPNPTLGQDAFAGRTFDGDLAR 760		705	Qy	
FVDFSTQRGLA-SDGRCKAFSARADGFALSEGVAAL 1731	AGGVTVMSDPYT	1685	Db	
FDPYSGAFCPITNELVKKTHLAVVÓDLALSÓCHCVFYGGÓVEGKNEKN 704	T	656	QУ	
VDGYQGLGNSASVLSGRIAYTFGWEGFALTVDTACSSSLVGIHLAMQALRRGECSLAL 1684		1627	Db	
RARIFOTTTQFMKVLVETRDYKIRFGLSEATHSMAL 655	ILDTLRARIFQT	615	Оy	
ITPREALAMDPQQRLMLETAWEAVERAGIDFUALKGTUTGVFVGMNGQSYMQLLACEAFR 1626		1567	Db	
KATMODTYRATLERLFIDLEQERLLDRGAPCSSEGLSSVTVDHPTFRR 614	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	567	Qy	
EQLWRVLAEGANLTIGEPADRGWDIGRLYHPDPDNPGTSYVDKGGFLTDAADFDPGFFG 1566	٦ –	1507	Db	
	PYLILR	552	QY	
-VEDHETVTALAQHLRAFLVSDADQAAVRVVSAADESEPIAIVGIGCREPGGIGS 1506	1	1453	Db	
RPVCAHTTVHRLRQRMPRFGQATRQPIGVFGTMNSQYSDCDPLGNYA 551		505	Qy	
ALRKRLSASTG1452	RAFSELGLUSLNAMALRKRL	1421	Db	
FSVDYLALICGFGAPLLARLLFYLERCDAGAFTGGHGDALKYVTGTFDSEIPCSLCEKHT 504		445	ΩY	
GGQAEAEPDS: GPTGEPAQRLAGLSPDEQQENLLELVANAVAE VLGHESAAEINVR 1420		1366	Db	
PNRFYQFAGPHIAANPQTDRDGHVLSSQSTGSSNTE 444	5 SGMTEAKDGGPGPSFNRFYQFAG	395	QУ	
PVLSEGFAATRP	AGPVSVAVADV DWPVLSEGFAATRP-	1331	σlα	

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NESULT 10
US-07-731-157A-7
Sequence 7, Application US/07731157A
Sequence 7, Application US/07731157A
Patent No. 5457032
GENERAL INFORMATION:
GENERAL INFORMATION:
MISSET, Onno
APPLICANT: Misset, Onno
APPLICANT: Van der Laan, Jan M.
APPLICANT: Lenting, Herman B.M.
INFLICANT: Lenting, Herman B.M.
ITITLE OF INVENTION: Mutated beta-lactam acylase genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IHM PC compatible
OPERATING SYSTEM: PC-DOS/MS DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
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TELEPHONE: 415 494 7622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 18 APR-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: EP 90200962
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591 LDRGAPCSSEGLSSVIVHHPTERRILDTLRARIEQTTTQFMKVLVETRDYKIREGLSEA- 649
                                       505 KIMERLYASPAFAVDDAAAIHADTLSPHYGLLKAKLEALGIQGSLPAEELROTLIAWDGR 564
                                                                                                                       45+ GEHEWRGWIPHEAMPR----VIDPPGGLIVTANNRVVADDHPDYLCTDCHP------PYRAE 504
                                                                                                                                                                      512 TVHRLR--
                                                                                                                                                                                                           399 ASTVAQLE - - - DATROWGLIDHNIVAGDVAGSIGHLVRARVPSRPRENGWLPVPGWS 452
                                                                                                                                                                                                                                                      458 APLIARLIFYLERCLAGAFTG GIL
                                                                                                                                                                                                                                                                                                                                            000
                                                                                                                                                                                                                                                                                                                                                                                  290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 AANALKERYDEXGQODIIGTEPEGVEAERLEADLAALRPAVDALLKAMGGDASDAAGGGSNN 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25H ARGAAHLAFDENHEGAV LPFDLTYTYFQSSSSGTTTARGARRNDVNSTSKPSPSGGFER 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: AMINO ACID
TOPOLOGY: 1200
HEROLOGY: 1200
HEROLOGY: 1200
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REFERENCE/LOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY
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                                                                RAE VENTER PH.D., BARHARA
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20.2%; Fred. No. 0.31,
utive 79; Mismatches 251; Indels 242; Gaps
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US-08-541-780-7
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Sequence 7, App...
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                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: GB
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-494-7622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                               ORIGINAL SOURCE:
                                                                                 MOLECULE TYPE: HYPOTHETICAL:
                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 18-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER PH.D., BARBARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
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TITLE OF INVENTION: Mutated beta-lactam acylase genes
NUMBER OF SEQUENCES: 50
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CLASSIFICATION: 435
                    STRAIN:
                                    ORGANISM:
                                                                                                                            TOPOLOGY:
                                                                                                                                                     TYPE:
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CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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Van der Laan, Jan M
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Query Match

1.7%; Score 106;

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                                                                                                                                                                                                                                    APPLICANT: NIWA, MINEO
APPLICANT: SAITO, YOSHIMASA
APPLICANT: FUJIMURA, TAKAO
APPLICANT: FUJIMURA, TAKAO
APPLICANT: NOGINCHI, YOSHINORI
APPLICANT: NOGINCHI, YUJI
TITLE OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 AANALKERYDDGGQDELCTFFGVEAERLEADLAALRPAVDALLKAMGGDASDAAGGGSNN 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    258 ARGAAHLAFUENHEGAV-LEPRITTYTYEQSSSSGTTTARGARKNDVNSTSKPSPSGGFEK 316
                                                           STREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VHGINIA
COUNTRY: USA
                                                                                                                                                                                   ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P \cap
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                             22202
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TELEX: 248855 OPAT UR
LNFORMATION FOR SEQ ID NO. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 774 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWAKE: Patentin kelease #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/633,760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                       575 YNAFKKALIKLVIDREGLEÓAISHPFAAVAPGVSPÓGQVWWAVPILLKUUDAGMIKGWSW 634
                                                                                                                                                                  520 DAAAIHADTLSP-----HVGLLRRRLEALGARDDSAAEGLRQMLVAWDGRMDAASEVASA 574
                                                                                                                                                                                                                   408 ATRGWGLIDHNLVAGDVAGSIGHLVRARVPSRPRENGWLPVPGWSGEHEWRGWIPHEAMP 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     413 YQFAGPHLAANPQTDRDGHVLSSQSTGSSNTEFSVDYLALICGFGAPLLARLLFYLERCD 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                383 PNSA------AKDGGPGPSFNRF 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           323 AADTALHAEVIFNTGIYEETPTDIKEWPMFIGMEGTLPRLNALGSYTARVAGVIGAMVFS 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      273 AV-LPPDITYTYFQSSSSGTTTARGAPRNDVNSTSKPSPSGGFEP-----PLAS---IM 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             160 RLG----------LLMGAVWFKLWRMLALPVVGAANALKLRYDDGGRD 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              217 SIGEGFVYPTPFYNTGLCHLIHDCVIAPMAVALRVRNVTAV----ARGAAHLAFDENHEG 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 LRAYVAGVNAFLASGA------PL-PVEYGLLGAE---PEPWEPWHSIAVMR 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162 FKEAVFMCNVFLHYGGLDIVHINHGDVIRIPLFPVQLFMPDVNRLVPDPFNTHH-----R 216
                                                                                                              609 HPTFRRILDTL---RARIEQTTTQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            299 HNGKVAYCVTHAFMDIHDLYLEQFAGEGRTARFGNDFEPVAWSRURIAVRGGADREFDIV 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  198 LLCIPPGAEADRLEADLATLRPAVDALLKAMGGDASDAAGGGSNNWAVAPGRTATGRPIL 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109 LTR---ACNAARERFGFSRCQGPPVDGAVETTGAE-ICTR-----LGLEPENTILYLVVTAI, 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER. IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 24
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 1.7%; Score 105; DB Local Similarity 20.7%; Pred. No. 0.39;
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                                                                                                                                                                                                                                                                          K---VIDPPGGLIVTANNKVVADDHPDYLCTDCHP-----PYKAERIMKKLVANPAFAVD 519
                                                                                                                                                                                                                                                                                                                                 RFGQATRQPIGVFGTMNSQY-----SDCDPLGNYAPY-----LILRKPGDQTE 564
                                                                                                                                                                                                                                                                                                                                                                                                                                         AGAPTG--GH----GDALKYVTGTFDSEIPGSLCSKHTPPVCAHTTVHPLP-----QPMP-521
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE: 774 amino acids
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APPLICANT: SAITO, YOSHIMASA
APPLICANT: FUJIMURA, TAXAO
APPLICANT: ISHII, YOSHIMOPI
APPLICANT: NOGUCHI, YUJI
TITLE OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE
NUMBER OF SEQUENCES: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
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REGISTRATION NUMBER: 24,618
REFERENCE/DOX'KET NUMBER: 18
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 01 MAY:1996
CLASSIFICATION: 4:35
ATTORNEY/AGENT INFORMATION:
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258 AGDPHRVFEI - - - PGTYAQHHLACDRFDM - TGL - - TVP - - -
                                                                                         198 LLCIPPGAEADRLEADLATLRPAYDALLKAMGGDASDAAGGGSNNWAVAPGRTATGRPIL 257
                                                                                                                                                                                                                                                                                       118 LRAYVAGVNAFLASGA-----
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                                          324 AADTALHAEVIENIGIYEETPIDIKEWPMFIGMEGTLPRLNALGSYTARVAGVIGAMVES 382
                                                                                                                                         273 AV LPPDITYTYFQSSSSGTTTARGAPPNDVNSTSKPSPSGGFER-----RLAS---IM 322
                                                                                                                                                                                                                                       217 STGEGFYYPTPFYNTGLCHLIIIQCYIAPMAVALRYRNYTAV----ARGAAHLAFDENHEG 272
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                                                                                                                                                                                                                                                                                                                                    162 FKEAVEMCNVFLHYGGLDIVHINHGDVIRIPLEPVQLEMPDVNRLVPDPFNTHH-----R 216
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TELEFAX: (703) 413-2220
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COMPUTER: 1HM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146; Conservative
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20.7%; Pred. No. 0.39;
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                                                                                                                                                                                        -LILMGSVWFKLWRMLALPVVGAANALKLRYDDGGRD 197
                                                                                                                                                                                                                                                                                    ----PL-PVEYGLLGAE---PEPWEPWHSIAVMR 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 774;
-GVPGFPHFA 298
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RESULT 14
US-08-931-608A-5
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INFORMATION FOR SEQ ID NO:
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HYPOTHETICAL:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 07601
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lobel, Peter APPLICANT: Sleat, David E.
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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411 Hackensack Ave, Continental Plaza, 4th Floor
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Best Local Similarity

Score 104.5, Pred. No. 0.3;

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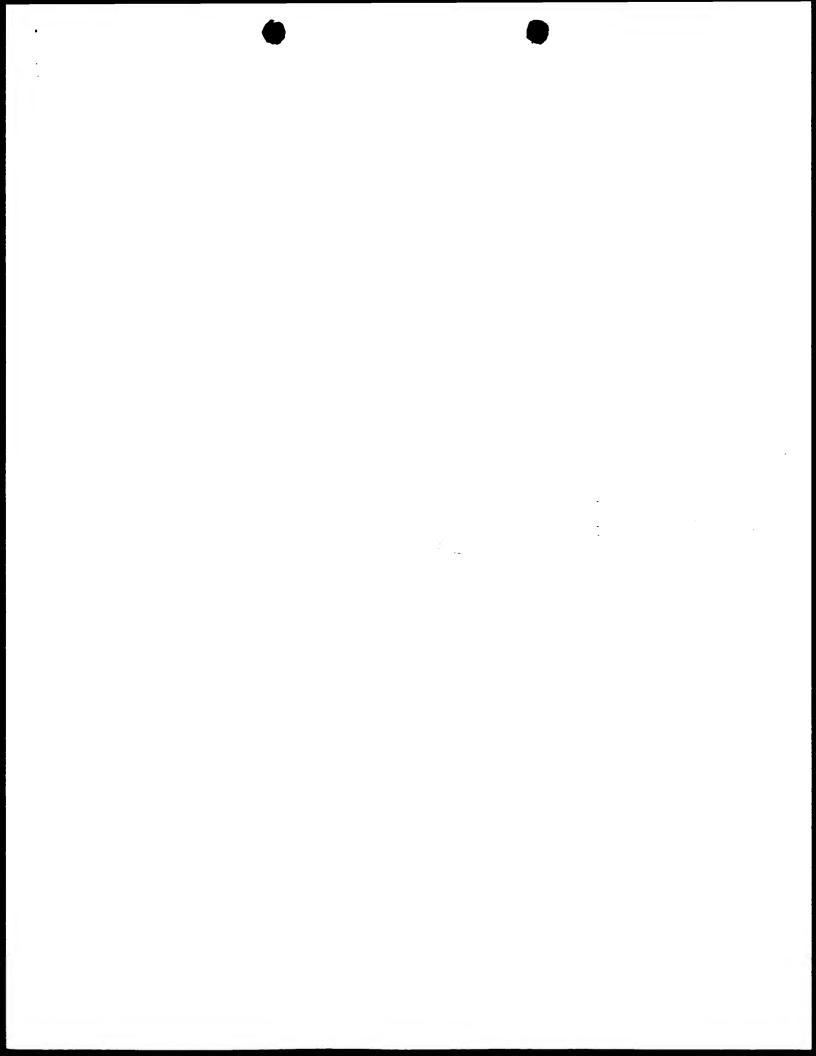
Length 635

Query Match

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ATTECK RI RI TELL TINFOR SFOR LU MOLL MOLL	COMING CO	RESULT 15 US-08-019-8 Sequence Patent No GENERAL APPLIC AP	y 245 b 10 b 304 y 3044 y 364 y 424 y 424 y 424 y 484 y 484 h 128 p 544 h 182 y 544 p 644 p 744 p	Matches
TALLER STATE	STATE: Virginia COUNTRY: U.S.A. ZIP: 22202 COMPUTER READABLE FORM: MEDIUM TYPE: Ficppy disk COMPUTER: 1BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTMARE: Patentin Release #1.0, Version #1.25 CIPRENT APPLICATION DATA: APPLICATION NUMBER: US/08/019,870 FILING DATE: 19930219 CIASS:HICATION: 435	T 15 -019-870-5 cont No. 5336613 meral information US/08019870 ent No. 5336613 meral information: APPLICANT: NIWA, MINEO APPLICANT: YOSHIMASA, SAITO APPLICANT: SASAKI, HITOSHI TITLE OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE MUMBER OF SEQUENCES: 42 CORRESPONDENCE ADDRESS: ADDRESSE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C. STREET: 1755 S. Jefferson Davis Highway, Suite 400 CITY: AT lington	MAVALHVKNVTAVARGAAHLAFDENH-EGAVLPPLITYTYFYSSSSGITTAKGAKKNUVN 303	s 77; Conservative 36; Mismatches 121; Indels 133; Gaps

5 Š ζ Сþ Ϋ́ Dβ νΩ US-08-019-870-5 Query Match 1.7%, Soure 104.5, DB 1, Length 774; Hest Local Similarity 21.7%; Pred No 0.44; Matches 91; Conservative 41; Mismatches 136; Indels 151; Gaps 372 VAGVIGAMVFSPNSA-----AK 401 635 VETRDYKIREG-----LSEA-------THSMALTFDPYSGAFCP 666 561 WDGRMDAASEVASAYNAFRRALTRLVTDRSGLEQAISHFFAAVAFGVSFQGQVWWAVFTL 620 608 ------DHPTFRRILDTL---RARIEQTTTQ-------FMKVI, 634 506 IMKRLVANPAFAVDDAAAIHADTLSP----HVGLLFFFLEALGARDUSAAEGLFQMLVA 560 554 ---LILRKPGIOTEAAKATMQDIYKATEERLETDEEQERLIJJRGA--PCSSEGUSSVIV- 507 454 EHEWRGWIPHEAMPR---VIDPPGGIIVTANNRVVADDHEDYLCTDCHP-----PYKAER 505 513 VHRLR------GRMPREGGATRQFIGVEGTMNSQY------SINTDPLGNYAPY---- 553 405 AGDVAGSIGHLVTVAQLYDA---TRG------WGLIDRARVPSRPRENGWLPVPGWSG 453 454 CGPGAPLLAKILEYLERCDAGAFTGGHGDALKYVTGTFD-SEIPCSLCEKHTRPVCAHTT 512 348 RGGADREFDIVETPHGPVIAGDP---RDGAALTLRSVQFAETDLSFDGLTRMPGASHNLV 404 402 DGGPGPSFNRFYQFAGPHLAANPQTDRDGHVLSSQSTGSSNTFFSVDYLA------1.1 453 288 VPGVPGFPHFAHNGKVAYCVTHAFMDIHDLYLEQFAGEGRTARFGNDFEPVAWSRDRIAV 347 621 LRDDDAGMLKGWSWDQALSEALSVASQNLTGRSWGEEHRPRFTHPLATQFPAWAGLLNP 679 19;

Search completed: March 28, 2003, 13:39:45 Job time: 42 secs



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A:Molecule type: DNA
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R:Teltord, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J. Virology 189, 304-316, 1992
                                                                                                                                                                                                                                                                             DNA-binding protein | equine herpesvirus 1 (strain Ab4p)
C:Species: equine herpesvirus 1
A:Note: host Equis caballus (domestic horse)
C:Date: 10 Sep-1992 #sequence_revision 30-Sep 1992 #text_change 16-Jul-1999
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A:Contents: annotation; possible protein-coding frames A; Note: neither amino acid nor nucleotide sequence is given C; Genetics:
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C:Superfamily: herpesvirus DNA-binding protein
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RGHPPGIDTPNPQWFWTLLQRNQMPARLLSKEDIETITAIKRFSDEYSAINFINLTPNNI 894
                                                                                                                                                                                                                                                                                                                                                                       SEATHSMALITEDPYSGAFCPITNFLYKRTHLAVVQDLALSQCHCVFYGQQVFGKNFKNQF 706
                                               RGMPPNSKSPNPQWFWTLLQRNQMPADKLTHEETTTTAAVKRETTEEYAATNETNLPPTCI 886
                                                                                                     RDLRVKNRVLFSNGGANMSEAARARVAGMASAYRRPDKGSNILNGAVGFLVKQYHGVLFP
                                                                                                                                                     PDIRVKNRVVESGNOTNUSEAAPARIVGLASAYQEQEKEVEMLHGALGELLKQEHCLLEP 826
                                                                                                                                                                                                                QPVLRRRFLDMLNGGF1TAKTVTVTVSDSGVLAPDLTRPASEPPTKDYDGDMARVSMEVL
                                                                                                                                                                                                                                                               QPVLRRRFVDLFNGGFISTRSITVILSEGPVSAPNPTLGQDAPAGRIFDGDLARVSVEVI 766
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C;Species: equine herpesvirus 4 (strain NS80567)
A;Variety: strain NS80567
C;Date: 11-Jan:2000 #sequence_revision 11 Jan:2000 #text_change 21-Jul-2000
C;Accession: T42574
R;Telford, E.A.; Watson, M.S.; Perrv. T. G.P.T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: 31
C:Superfamily: herpesvir
C:Keywords: DNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R:Telford, E.A.; Watson, M.S.; Perry, J.; Cullinane, A.A.; Davison, A.J. J. Gen. Virol. 79, 1197-1203, 1998
A:Title: The DNA sequence of equine herpesvirus-4.
A:Reference number: Z22173; MJID:98264497; FMID:9603335
A:Accession: T42574
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Pesidues-1-1208 <TEL>
A:Cross: references EMBL AF938027. NID:92605950; PIDN.AAC59547 1, PID:929
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                                                                                                              VIAPMAVALRYRNYTAVARGAAHLAEDENHEGAVLPPDITYTYFQSS--SSGTTTARGAR
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                                                                                          RTMDAQTNMGVVSTGDG-----AFDFGACVGDANQSSTTFNMGPA--SSSAPAGQKRFH 1185
                                                                                                                                    KILDEKT----TAGDGETPTNLAFNFDSCEPSHDTTSNVLNISGSNISGSTVPGLKRPP 1181
                                                                                                                                                                                    TAVFSVVLTALGARTQHLAVDDWIGLVDDEFLAASLDALNAAVVDQF-GEWSVEAAQDMI 1133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RDIRVKNRVVFSGNCTNLSEAARARLVGLASAYQRQEKRVUMLHGALGFLLKQFHGLLFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RGHPPGIDTPNPQWFWTLLQRNQMPARLLSKEDIETITAIKRFSHEYSAINFINLTPNNI 894
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C:Accession: A28601
R:Gao, M.: Bouchey, J.; Curtin, K.: Knipe, D.M.
Virology 163, 319-329, 1988
Virology 163, 319-329, 1988

of a portion of the herpes simplex virus ICP8

protein

#text_change 16-Jul-1999

DNA-binding protein - human herpesvirus 1 (strain KOS1.1) C;Species: human herpesvirus 1 A;Note: host Homo sapiens (man) C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_

RESULT 4

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A;Accession. A28601
A;Molecule type: DNA
A;Residues: 1-1196 <GAO>
A:Cross reterences: GB-M20165; NID:g340120; PIDN:AAA45793.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Geneties:
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                                                         827 KIMPPNSKSPNPQWFWTLLQRNQMPADKLTHEEITTIAAVKRFTEEYAAINFINLPPTCI 886
                                                                                                                                                                                                                                                                                                                                                                                                        648_EATHSMALTFDPYSGAFCPITNFLVKFTHLAVVQDLALSgc:ncvffygggvBgffnffngfq_707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             470 ERCINGATIVGRQEMOVERYVADSNOTOVPCNI.CTFDTRHACVHTTILMRI.RARHPKFASAA 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    411 PGTHVAANPQVDREGHVVPGFEGRPTAPLVGGTQ-EFAGEHLAMLCGFSPALLAKMLFYL 469
                                                                                                                                                                                                                                                                                                                                                                        649 EANHAMSLTLDPYACGPCPLLQLLGRRSNLAVYQDLALSQCHGVFAGQSVEGRNFRNQFQ 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               589 LQYVDQAVPTAMGRLETIITNREALHTVVNNVRQVVDREVEQLMRNLVEGRNFKFRDGLG 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       469 ERCDAGAFTGGHG-DALKYVTGTFDSEIPCSLCEKHTRPVCAHTTVHRLRQRMPRFGQAT 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           452 DTAAARANAVGAYLARAAGLVGAMVESTNSALIILTEVDDAGPADPKDIISK-PSFYRFFLY 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         296 GARRNDVNSTSKPSPSGGFERRLASIMAADTALHAEVIFNTGIYEETPTDIKEWPMFIGM 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176 GGLDIVHINHGDVIRIPLEPVQLEMPDVNRLVPDPENTHHRSIGEGEVYPTPEVNTGLCH 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MENTOKTVT----VPTOPLOYVY--ACRVEDLDLEEISFLAARSTDSDLALLPIMRNLIVE 55
                                                                                                                                                                                                                                                                                    PVLKRRFVDLFNGGFISTBSITVTLSEG-PVSAPNPTLGQDAPAGRTEDGDLARVSVEVI 766
NGKPPGSNÖPNPOWFWTALORNOLPARILSREDIETTAFIKKESLDYGAINFINLAPNNV 888
                                                                                                                                                                                 RDIRVKNRVVFSGNCTNI.SEAARARI.VGI.ASAYQRQEKRVDMI.HGALGFILI.KQFHGI.I.FP 826
                                                                                                                                                                                                                                              PVLRRRVMDMFNNGFLSAKTLTVALSEGAATCAPSLTAGQTAPAESSFEGDVARVTLGFP 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RQPIGVEGTMNSQYSIKOPIGNYAPYLILRKPGDQTEAAKATMQDTYRATLERLFIDLEQ 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGR-----DGGGKGPAGGFEQRLASVMAGDAALALESIVSMAVFDEPPTDISAWPLCEGQ 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARRHFGFSDYTEREGDI.KHETTGEAI.CERI.GI.DPDRAII.YI.VVTEGFKEAVCI.NNTFI.HI 178
                                                                                                                          KELRVKSRVLFAGASANASEAAKARVASLQSAYQKPDKRVDILLGPLGFLLKQFHAAIFP 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ERTIDEGAPOSSECTSSVIVDHPTERRICDTLRARTEQTETQFMKVLVETERDYKTREGLS 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RGAIGVFGTMNSMYSDCDVLGNYAAFSALKR-ADGSETARTIMQETYRAATERVMAELET 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGPHLAANPOTDRIGHVI.----SSQSTGSSNTEFSVDYLALICCFGAPILLARILFYL 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGTLPRLNALGSYTARVAGVIGAMVFSPNSALYLTEVEDSGMTEAKDGGPGPSFNRFYQF 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLFEAVVGPAAVALRCRNVDAVARAAAHLAFDENHEGAALPADITFTAFEASQG--KTPR 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGSDKVTIGGAEVHRIPVYPLQLFMPDFSRVIAEPFNANHRSIGENFTYPLPFFNRPLNR 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARERFGFSRCQGPPVGGAVETTGAEICTRLGLEPENTILYLVVTALFKEAVFMCNVFLHY 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGFEANVAVVVGSRTTGLGGTAVSLKLTPSHYSSSVYVFHGGRHLDPSTQAPNLTRLCER 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                METKPKTATTIKVPPGPLGYVYARACPSEGIEL - - LALLSARSGDADVAVAPLVVGLTVE 58
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C;Superfamily: herpesvirus DNA-binding protein
C;Keywords: DNA binding
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A;Residues: 1-1196 <MCG>
A;Cross:references: GB:D10879, NID g221721; PIDN BAA01675 1; PID g221750; GB D00317
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A;Residues: 1-1196 <QUI>
A;Residues: 1-1196 <QUI>
A;Cross references: GB X03181, GB.M12356; NID-959862; PIDN CAA26940.1, FID 959863
A;Experimental source: strain 17
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Nucleic Acids Res. 13, 8143-8163, 1985
A;Title: DNA sequence of the region in the genome of herpes simplex virus type 1 cont
A;Reference number: A93601; MUID:86067223; FMID:2999714
A;Accession: A03790
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Note: host Homo sapiens (man)
C;Date: 04-Dec-1986 **sequence_revision 04-Dec-1986 **text_change 16-Jun-2000 C;Accession: A03790; B30085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               major DNA-binding protein UL29 - human herpesvirus 1 (strain 17)
C;Species: human herpesvirus 1
                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1007 LNGGKNVCPLFTFDRTRRFIIACPRGGFICPVTGPSSGNRETTLSDQVRGIIVSGGAMVQ 1066
119 ARRHEGESDYTPRPGDLKHETTGEALCEKLGLDEDRALLYLVVTEGEKEAVCINNTELHI. 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       947 KALLEKTENLPELWTTAFTSTHLVRAAMNQRPMVVLGISISKYHGAAGNNRVFQAGNWSG 1006
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                                                                                                                                           59
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                 1 MENTOKTVT----VPTGPLGYVY--ACRVEDIDLEEISFLAARSTDSDLALLPLMRNLTVE 55
                                                                     ARERFGFSKCGGPPVDGAVETTGAEICTRLGLEPENTILYLVVTALFKEAVFMCNVFLHY 175
                                                                                                                                                                                                         KTETSSLAVVSGARTTGLAGAGITLKLTTSHEYPSVEVEHGGKHVLPSSAAPNLTRAGNA 115
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                                                                                                                                    SGFEANVAVVVGSKITGLGGTAVSLKLIPSHYSSSVYVFHGGRHLDPSTQAPNLITRLCER 118
                                                                                                                                                                                                                                                                                   METKPKTATTIKVPPGPLGYVYARACPSEGIEL--LALLSARSGDSDVAVAPLVVGLTVE 58
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                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative 199; Mismatches 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            48.4%; Score 3049; DB 1;
49.8%; Pred. No. 4.4e-223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1196
                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 48; Gaps
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1007
1174 FHGDDPFG-EGPPDKKGDLTLDM 1195
                                                                          1181 PEDDELFDLSGIPIKHGNITMEM 1203
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                                                                                                                                                                  HEAEALVSQLGNAGE: · · · · · · · VENEGUEGCE · · · · · DDNATFEGGPGAPGPAFAGRKRA 1173
                                                                                                                                                                                                                                                                                                                                                                                                                            LAIYATVVRAVGARAQHMAFDDWLSLTDDEFLARDLEELHDQIIQTLETPWTVEGAL--- 1123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LMGGKNACPLLIFDRTRKFVLACPRAGFVCAASSLGGGAHESSLCEQLRGIISEGGAAVA 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LNGGKNVCPLFTFDRTRRF11ACPRGGF1CPVTGPSSGNRFTT1,SDQVRG11VSGGAMVQ 1066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RALMDAVDAHPGAWTSMFASCNELFPVMAARPMVVLGLSISKYYGMAGNDRVFQAGNWAS 1005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GELAQFYMANLILKYCDHSQYLINTLTSIITGARRPRDPSSVLHWIRKDVTSAADIETQA 946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NGKPPGSNQPNPQWFWTALQRNQLPARLLSREDIETTAFIKKFSLDYGAINFINLAPNNV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILEVKNRVVFSGNCTNLSFAARARLVGLASAYQRQEKRVDMLHGALGFLLKQFHGLLFD 826
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                                                                                                                                                                                                                                                                                                                                                  SSVEVATVKSLGPKTÖQLÖJEDWIALLEDEYLSEEMMELTARALERGNGEWSTDAALEVA 1125
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A:Molecule type: DNA
A:Residues: 1-1196 <HAM>
A:Cross-references: GB:M21629
C:Superfamily: herpesvirus DNA-binding protein
C:Keywords: DNA binding
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A:Note: host Homo sapiens (man)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 07-Jun-1996
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A;Title: Conservation of a gene cluster including glycoprotein B in bovine herpesviru A;Reference number: A94381; MUID:88306231; PMID:2841793
A;Accession: D29242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: D29242
R;Hammerschmidt, W.; Conraths, F.; Mankertz, J.; Pauli, G.; Ludwig, H., Buhk, H.J.
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                                                      708 PVLRRRFVDLFNGGFISTRSITVTLSEG-PVSAPNPTLGQDAPAGRTFDGDLARVSVEVI 766
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 48.4%; Score 3047; DB 1; Local Similarity 49.8%; Pred. No. 5.3e-223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 METKPKTATTIKVPPGPLGYVYARACPSEGIEL - LALLSARSGDSDVAVAPLVVGLTVE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MENTQKTVT---VPTGPLGYVY--ACRVEDLDLEEISFLAARSTDSDLALLPLMRNLTVE 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGTLPRLNALGSYTARVAGVIGAMVFSPNSALYLTEVEDSGMTEAKDGGPGPSFNRFYQF 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GER-----DGGGKGAAGGFEQRLASVMAGDAALALESIVSMAVFDEPPTDISAWPLFEGQ 351
PVLRRRVMDMFNNGFLSAKTLTVALSEGAAICAPSLTAGQTAPAESSFEGDVARVTLGFP
                                                                                                                                                                                                                                                                                                                                                                                                   ROPIGVEGIMNSOYSDCDPLGNYAPYLILKKPGDQTEAAKATMQDTYRATLERLETDLEQ 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPCDAGAFT/GHG-DALKYVTGTFDSEIPCSLCEKHTPPV/AHTTVHPLPQRMPRFGQAT 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGPHLAANPOTDRDGHVL-----SQSTGSSNTEFSVDYLALICGFGAPILLARILFYL 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DTAAARANAVGAYLARAAGLVGAMVFSTNSALHLTEVDDAGPADPKDHSK-PSFYRFFLV 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GARRNDVNSTSKPSPSGGFERRLASIMAADTALHAEVIFNTGIYEETPTDIKEWPMFIGM 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   {\tt LLFEAVVGPAAVALRCRNVDAVARAAHLAFDENHEGAALPADITFTAFEASQG--kTPR}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIHDCVIAPMAVALRVRNVTAVARGAAHLAFDENHEGAVLPPDITYTYFQSSSSGTTTAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGSDKVTIGGAEVHRIPVYPLQLFMPDFSRVIAEPFNANHRSIGEKFTYPLPFFNPPLNR 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGLDIVHINHGDVIRIPLFPVQLFMPDVNRLVPDPFNTHHRSIGEGFVYPTPFYNTGI,CH 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARRHEGESDYTPRPGDLKHETTGEALCERLGLDPDRALLYLVVTEGEKEAVSINNTFLHL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ARERFGFSRCQGPPVDGAVETTGAEICTRLGLEPENTILYLVVTALFKEAVFMCNVFLHY 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGFEANVAVVVGSPTTGLGGTAVSLKLTPSHYSSSVYVFHGGPHLDPSTQAPNLTRLCER 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KTFTSSLAVVSGARTTGLAGAGITLKLTTSHFYPSVFVFHGGKHVLPSSAAPNLTRACNA 115
                                                                                                                EANHAMSLITLDPYACGPCPLLQLLGRRSNLAVYQDLALSQCHGVFAGQSVEGRNFRNQFQ
                                                                                                                                                                       EATHSMALTFDPYSGAFCPITNFLVKRTHLAVVQDLALSQCHCVFYGQQVEGRNFRNQFQ 707
                                                                                                                                                                                                                                                                                        ERLIJDRGAPCSSEGLSSVIVDHPTERRILDTLRARIEOTTTQFMKVLVETRDYK1REGLS 647
                                                                                                                                                                                                                                                                                                                                                  RGAIGVFGTMNSMYSDCDVLGNYAAFSALKR-ADGSETARTIMQETYRAATERVMAELET 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ERCDGAVIVGRQEMDVFRYVADSNQTDVPCNLCTFDTRHACVHTTLMRLRARHPKFASAA 529
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Oy 182 HINHGDVIRIPLEPVQLEMPDVNRLVPDPENTHHRSIGEGFVYFTPFYNTGLCHLIHDCV 241	QY 122 FSRCQGPPVDGAVETTGAEICTREGLEDENTILYLVVTALFKEAVFMCNVFLHYGGLDIV 181	OY 62 LAVVSGARTTGLAGAGITIKITTSHFYDSVFVFHOGKHVLDSSAADNLTRACNAARERFG 121 ; 1 1 1 1 1 1 1 1 1	OY 4 TOKTVIVPTGPLGYVY AGPVEDLDLEFISFLAARSIDSDLAKLFLMRNLTVEKTFISS 61 	Overy Match 47.7%; Score 3003; DB 1; Length 1197; Hest Local Similarity 48.9%; Pred No 1.4e-219; Matches 594; Conservative 212; Mismatches 369; Indels 40; Gaps 16;	Map position: 0.375-0.405 C)Supertamily: herpesvirus DNA-binding protein C;Keywords: DNA binding; zinc finger F;499-512/Region: zinc Linger	A;Moltecule type: DNA A;Residues: 1-1197 -ToH. A;Note: sequence extracted from NCBI backbone (NCBIN.129069, NCBIP.129070) Genetics:	<pre>19, 183-196, 1993 ptide sequence of the ma pber: A48350; MOID:93228 ptide sequence of the ma ptide sequence of the m</pre>	HOP	RESULT 7 A48350 UNA-binding protein - human berpesvirus 2 C)Species: human herpesvirus 2	1174		SSYFVATVKSLGPHTQQLQIEDWLALLEDEYLSBEMMELTARALERGNGEWSTDAALEVA - EAVKILDEKTTAGDGETPTNLAFNFD SGEPSHDTTSNVLNISGSNISGSTVPGLKRP	OY LOOK LAKKANAN ELETERRIETEN PRISETEN FURKESINETELSDORG LIVEGANAO 1066			829 NGKPRGSNOPNPOWFWTALORNOLPARLISREDIETTAPIKKESLDYGAINEINLAPNNV 829 NGKPRGSNOPNPOWFWTALORNOLPARLISREDIETTAPIKKESLDYGAINEINLAPNNV 887 GELAOFYMANIJILKYCDHSQYIJNTIJSITTGAKKPRDPSSVIJWIRKDVTSAADIETOA	1	QY 767 RDIRVKNRVVESGNCTNLSEAAFAFLYGIASAYQRQEKEVDMLHGALGELLKQEHGLLEP 826
RESULT 8 DNBEBG	Qy 1189 LSCIPIKHONITMEM 1203	1132 V	10/3 VKAVGARAQHAFDUWUSLIDUEFIARDLEELHIQIIQIIJETIWIVEGAL:EAVKI	1013 VCPLETFDRTRREIIACPRGGFICPVTGPSSGNRETTLSDQVRGIIVSGGAMVQLAIYAT	QY 953 TENLPELWTTAETSTHLVRAAMNQRPMVVLGISISKYHGAAGNNRVFQAGNWSGINGGKN 1012 :	Qy 893 YMANLILKYCDHSQYLINTLTSIITGARRPRDPSSVLHWIRKDVTSAADITTQAKALLEK 952 	OY 833 SKSPNPQWFWTLLQRNQMPADKLTHEEITTIAAVKKETEEYAAINFINLPPICIGELAQE 892 K VIE	QY 773 NRVVESGNCTNLSBAARARLVGLASAYQRQEKRVDMLHGALGELLKQFHGLLFPRGMPPN 832	OY 714 FVDLFNGGFISTRS!TVTLSEG-PVSAPNPTLGQDAPAGRTFDGDLARVSVEVIRD!RVK 772	Qy 654 ALTEDPYSGAFCPITNFLVKBTHLAVVQDLALSQOHOVPYSGAVESBNIFNQFGPVLRRR 713 : : : : : : :	OY 594 GAPCSSEGLSSVIVDHPTFRRILDTLRARIEQTTTQFMKVLVETRDYKIREGLSEATHSM 653	Qy 534 FGTMNSQYSDCDPLGNYAPYLILRKPGDQTEAAKAIMQDTYRATLERLFIDLEQERLLDR 593		Qy 422 ANPQTDRDGHVLSSQSTGSSNTERGVDYLALICGFGAPLLARLLFYLERCDAG 474	OY 362 LNALGSYTARVAGVIGAMVESDNSALYLTEVEDSGMTEAKDGGDGDSFNRFYOFAGDHIA 421	Qy 302 VNSTSKPSPSGGFERRLASIMAADTALHAEVIFNTGIYEETPTDIKEWPMFIGMEGTLPR 361	Oy 242 IAPMAVALRVRNVTAVARGAAHLAFDENHEGAVLPPDITYTYFOSSSSGTTTARGARRND 301 :	Db 185 TIGDAEVHRIPVYPLQMFMPDFSRVTADPFNCNHRSIGENENYPLPFFNRPLARLLFEAV 244

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A;Molecule type: DNA
A;Residues: 1-1186 <HAM>
A;Cross-reterences: GB:M21628
C.Supertamily. herpesvirus DNA-binding protein
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A;Title: Conservation of a gene cluster including glycoprotein B in bovine herpesvirus A;Reference number: A94381; MUID:88306231; PMID:2841793
A;Accession: A29242
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C;Species: bovine herpesvirus 2
C;Date. 31 Mar 1990 #sequence_revision 31-Mar-1990 #text_change o7-Jun-1996
C;Accession: A29242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                             RVKNRVVFSGNCTNLSEAARARLVGLASAYQRQEKRVDMLHGALGFLLKQFHGLLFPRGM 829
                                                                                            RRRVLDMFNNGFLSARTLTVALTDGACISAPGLVSGQHAAAESGFEGDVARVNLGFPKEI 767
                                                                                                                                                                                                                     HAMSLTLDPHASVPCPLLQMLGRRSNLAVYQDLALSQCHGVFEGQAVEGRNFRSQFQPVL
                                                                                                                                                                                                                                                                                 HSMALTFDPYSGAFCPITNFLYKRTHLAVVQDLALSQCHCVFYGQQVEGRNFRNQFQPVL 710
                                                                                                                                                                                                                                                                                                                                                                                                           LDRGAPCSSEGLSSVIVDHPTFRRILDTLRARIEQTTTQFMKVLVETRDYKIREGLSEAT 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DGGVILGRPEMDTFKYVSDSAHTDVPCCLCSLDNPHSCAHTTLLRLPARHPKFTSTTRGA 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DAGAFTG-GHGDALKYVTGTFDSEIPCSLCEKHTRPVCAHTTVHRLRQRMPRFGQATRQP 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAARAASIGAYLGRAAGLVGAMVFSSNSALHLTEVDDAGPADPKD-PTKPSFYRFFLVPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HRNPREC----GGGFEQRLASVMAGDAALALESIMSMAVFEEPPTDIGTWPMLTCQES 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RRNDVNSTSKPSPSGGFERRLASIMAADTALHAEVIFNTGIYEETPTDIKEWPMFIGMEG 357
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                                                                                                                                                              RRRFVDLFNGGFISTRSITVTLSEGP-VSAPNPTLGQDAPAGRTFDGDLARVSVEVIRDI 769
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                                                                                                                                                                                                                                                                                                                                                   IDAAVPTSPAKLESIITGREALQTVVSNVKQVVDGEVAQLMRALVEGRGFRFREALGEAN 647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IGVFGTMNSQYSDCDPLGNYAPYLILRKPGDQTEAAKATMQDTYRATLERLFIDLEQERL 590
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A:Residues: 1-375 <BEL>
C:Superfamily: herpesvirus DNA-binding protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C:Accession: JQ0846
R:Bell, C.W.; Whalley, J.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UNA-binding protein - equine herpesvirus 1 (fragment)
C;Species: equine herpesvirus 1
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 23-Feb-1997
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Best Local :
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                                                           1128 ILDEKTTAG---DGETPTNLAFNFDSC---EPSHDTTSNVLNISGSNISGSTVPGLKRPP 1181
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                                                                                                                                                                                                                                                      182
301 NMEAQTTAGAVAAGEG----AFDFGACVGDTPQQSTSA----FNGGLAMAAAPAGQKRSL 352
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                                                                                                                                                                                        AIYATVVRAVGARAQHMAFDDWLSLTDDEFLARDLEELHDQIIQTLETPWTVEGALEAVK 1127
                                                                                                                                                                                                                                                NGGKNVCPLMAFERTEREVLACERVGFTCEAGGEGTGVENILSEQVRGIVSEGGTMVQT 241
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                                                                                                                                                                                                                                                                                                              NGCKNVCPLFTFDRTRRFITACPRGGFTCPVTGPSSGNRFTTLSDQVRGTTVSGGAMVQL 1067
                                                                                                                                                                                                                                                                                                                                                                             EVLQRLGSNPAAWTGTFTSTNMVRYVMDQRPMVVIGLSISKYNGSAGNNRVFQAGNWNGL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELAGEYFANLVLKYCDHSQYFINGLTAIVVGSRRPKDPAAVLAWIDKTINGAADVEFAAQ 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.4%; Score 1094.5; DB 2; Length 375; 55.5%; Pred. No. 3.5e-75;
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A:Residaus: Televences: EMBL:V01555; NID:q59074, PIDN:CAA24808.1, PID.q1334916
A:Cross-reterences: EMBL:V01555; NID:q59074, PIDN:CAA24808.1, PID.q1334916
Hacer, R.: Hankler, A.T.: Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.;
ture 410, 207-211, 1984
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Mol. Biol. Med. 1, 21-45, 1983
Mol. Biol. Med. 1, 20-45, 1983
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C:Species: human herpesvirus 4, Epstein-Harr virus
C:Date: 25 Feb: 1985 #sequence_revision 25-Feb:1985 #text_change 16-Jul-1999
C:Acression: A4:045; A0:3791: S:33057
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                                                                                                          476 FPPVMST@RRDPYVISGASGSYNETDFLGNFLNFIDKEDDGQRPDDEPRYTYWQLNQNLL 535
                                                                                                                                                                                                                                                                                                                                            424 YLQFCQ------GQKSSLTPVPETGSYVAGAAASPM-CSLCEGRAPAVCLNTLFFRLRDR 475
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ATLERLFIDLEOFMILIPMAPMSSEGI.SSVIVDHPTFRRILDTLRARIEQTTTQFMKVLV 635
                                                                                                                                                                                                                                 MPREGOATROPLICVECTMNSQYSDCDPLGNYAPYLLL...--RKPGDQTFAAKATMQDTYR 575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KVAALHRYNASI.APHVSTOTEATNSVLYV-----SGVSKSTGQGKESLENSEYMTHGLGT-370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHLAANPQTDRDGHVLSSQSTGSSNTEFSVDYLALICGFGAPLLARLLF 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALMIVUSAACELAVSYAPAMLEASHETPASLNYDSWPLFADCEGPEA 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.6%; Score 669; DB 1; Length 1128; 23.2%; Pred. No. 5.1e-42; tive 186; Mismatches 537; Indels 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---GLDPSAYLGAVAITEAFKERLYSGNLVAIPSLKQEVAVGQS 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VELLEKQSLQDQAKVAKVAPLKEFPAST 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246;
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C;Accession: T42922
R;Albrecht, J.C.; Fleckenstein, B.
submitted to the EMBL Data Library, August 1998
submitted to the Fimary structure of the herpesvirus ateles
                                                                                                               C; Superfamily: herpesvirus DNA-binding protein
                                                                                                                                          A;Rcsiducs: 1:1128 <ALB>
A;Cross-references: EMBL:AF083424; PIDN:AAC95531.1
A;Experimental source: strain 73
                                                                                                                                                                                                                          A:Status: preliminary: translated from GB/EMBL/DDBJA:Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Variety: strain 73
C:Date. 21-Jan-2000 #sequence_revision 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Species: ateline herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         major single stranded DNA binding protein
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                                                                                                                                                                                                                                                                                       A; Accession: T42922
                                                                                                                                                                                                                                                                                                                     A; Reference number: Z22274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
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     Matches 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1127 E 1127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1071 L----EGVWGGPGAAQUNFISVAEPVSTASQASAGLLLGGGGGGGGGGGPKRPLATVLPGL 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1016 CNLVDAMGEACA-----SUTRDDAEYLLGRESVLADSVLETLATIASSGIEWTAEAARDF 1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              743 TTRRENYI--INGPYMKFLNTYHKTLF----PDTKLSSLYLWHNFSRRRSVPVPSGASA 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 690
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                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VRAVGARAQHMAFDDWLSLT--DDEFLARDLEELHDQIIQTLET-----PWTVEGALEA 1125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NQRPMVVLGISISKYHGAAGNNRVFQAGNWSGINGGKNVCPLFTFDRTRRFTTACPRGC- 1033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VKILDEKTTAGDGETPTNLAFNFDSCEPSHDTTSNVLNISGSNISG-----STVPGL 1177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIQSVPARDYPHVLG--TRAVESAA-----AYAEATSSLIAT-TVVCAATDCLSQVC 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EEITTIAA-VKRFTEEYAAINFINLEPTCIGELAQEYMANLILKYCDHSQYLINTLTSII 916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YORQEKRYDMLHGALGFLLKQFHGLLFPRGMPPNSKSPNPQWFWTLLQRNQMPADK-LTH 857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PDIDAALQGRVYGRRLPVRMSKVLML^PRNIKIKNRVVFTGENAALQNS-----FIKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     K-NNITYKDLVKSCYHVMQYSCNPFAQPACPIFTQLFYRSLLTILQD1SLP1CMC----- 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RKQAGGSSMRKKEVEATPTLGLTVKRRTQAATTYETENTRAGLEATTSQKQEEDGVFDVV 1015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KARPVVTLPVTINKYTGVNGNNQIFQAGN-LGYFMGRGV-----DRN---LLQAPGAGL 955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EEYSDLALFYDGGSRAHEESNYIDYYPGNLYTYAKQRLNNAILKACGQTQFYISLIQGLV 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----QDAPAGRTFDGDLARVSVEVIRDIRVKNRVVFSGNCTNLSEAARARLVGLASA 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QVEGRNFRNQFQPVLRRRFVDLFNGGF----ISTRSITV-----TLSEGPVSAPNPTLG- 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --TGARRPRDPSSVLHWIRKDVTSAADIETQAKALLEKTENLPELWTTAFTSTHLVRAAM 974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ETRDYKIREGLSEATHSMALTEDPYSGAFCPITNFLVKRTHLAVVQDLALSQCHCVFYGQ 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -YEND-NPGLGQSPPEWLKGHYQTLCTNFRSLAIDKGVLTAKEAKVVHGEFTCDL 689
  Conservative 194, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --FICPVTGPSSGNR-ETTLSDQVRGIIVSGGAMV-----QLAIYATV 1073
                          10.1%; Score 633; DB 2; 22.4%; Pred, No. 2.8e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----RDFVKMFKDVDAAVDAEVVQFMNSMA 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ateline herpesvirus 3 (strain 73)
     514; Indels 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         #text_change
                                                       Length 1128;
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Caps
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11 PTGPLGYVYACRVEDLDLEEISFLAARSTDSDLALLPLMRNLTVEKTFTSSLAVVSGART 70

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Qy Qy Qb

GFR GAM :	GYEMGRGVDRNLIPDSSTLSDQVRGI1VSGTLSDQVRGI1VSGKNVQTIFDDKDNLNIFE	908 1021 958	
ENLPELWITAF :: !!LKEDIATIG- KNVCPLFT-FD	RKDYTSAADIETQAKALLEKTI :::	913 855 965	
PYLINTL-	LTHEEITTIA-AVKRFTEEYAAINFINLPPTCIGELAGFYMANLILKYCDHSQYLINTL-::	855 795	
IQMPA-DK : QIPVLPG	YOROEKRYDMLHGALGFULKOFHGILFPRGMPPNSKSPNPQWFW-TLLORNQMPA- 	799 743	
ARLVGLASA 	APNPTLGQDAPAGRTFDGDLARVSVEVIRDIRVKNRVVESGNCTNLSEAARAR	739 695	
LSEGPVS	QVEGRNEKN	696 651	
SMGMMPSE	SEATHSMALTFDPYSGAFCP)TNFLVKRTHLAVVQDLALSQCHCVFYGQ	647 593	
YKIREGL : INFRETI	RLLDKGAPCSSEGLSSVIVDHPTFRRILDTLRARIEQTTTOFMKVLVETRDYKIREGL	589 539	
FIDLEQE	VEGIMNSQYSDODPLGNYAPYLILRKPGDQTEAAKAIMQDIYRAILERLE	533 489	
ATROPIG : : SQRRDPY	AGAFTGGHGDALKYVTGTFDSEIPCSLCEKHTRPVCAHTTVHRLRORMPRFGQATROP1G	473 429	
.FYLERCI : :: !YYMQFCQ	YOFAGPHLAANPQTDRDGHVLSSQSTGSSNTEFSVDYLALIGGEGAPLLARLLFYLERGD:	413 369	
GPSFNRF : :	IGMEGTLPRLNALGSYTARVAGVIGAMVESDNSALYLTEVEDSGMTEAKDGGDGDSFNRE	353 312	
TDIKEWPMF : EPCALLDYTSWPIF	KPSPSGGFERRLASIMAADTATUAEVIFNTGI-YEETPTU	307 260	
NDVNSTS	VALRVRNVTAVARGAAHLAFDENHEGAVLPPDITYTYFQSSSSGTTTARGARRNDVNSTS	247 227	
CVIAPMI : : ! SLFTS!!	DVIRIPLFPVQLFMPDVNRLVPDPFNTHHRSIGEGFVYPTPFYNTGLCHLIHDCVIAPMA : :: : : : : : : : : : : :	187 186	
IVHINHO	DGAVETTGAEICTRIGLEPENTILYLVVTALFKEAVFMCNVFLHYGGLDIVHINHG	131 131	
RCQGPPV SFT-PRH	TGLAGAGITLKLTTSHFYPSVFVFHGGKHVLPSSAAPNLTRACNAARERFGESRCQG	71 78	
CAVHKKII	PVGACGYIYVYPKEGFPFQEASLLGNRNVGADAMSLPLLSGLTVEANFSFNVKAVHKKID	18	

200

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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1995
C;Superfamily: herpesvirus DNA-binding protein
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C;Species: equine herpesvirus 2
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 26-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-1145 <TEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Mol. Biol. 249, 520-528, 1995
A;Title: The DNA sequence of equine herpesvirus 2.
A;Reference number: S55594; MUID:95302501; PMID:7783207
A;Accession: S55600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1018 IEL·····VKGLGESCENMTEDDLQFYLGDYYIMSDEIWSRFQLLTDSGTPWSVE···S 1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1065 VQLAIYATVVRAVGARAQHMAFDDWLSLTDDEFLARDLEELHDQIIQTLETPWTVEGALE 1124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1125 AVKILDEKTTAGDGETPTNLAF 1146
                                                     495 PYVVTGVAGA-YNDLDIAGNFANY---RDKDEESNQSEEREKFTYWQVTQTVL----ER 545
                                                                                                           530 PIGVFGIMNSUYSDCDPLGNYAPYLILRKPGDQTEAAKAIMQDIYRATLERLFIDLEQER 589
                                                                                                                                                                   435 AQHQKSSNNSGYNVPTYVGTAANTPMCELCRGSCPASCVNTLFYRLRDRFPPVVASVRRD 494
                                                                                                                                                                                                                      471 CDAGAFTGGHGDALKYVTGTFDSEIPCSLCEKHTRPVCAHTTVHRLRQRMPR-FGQATRQ 529
                                                                                                                                                                                                                                                                               378 HGLACLAEPTQKENGLESFPGVPASALSGSN---YSLHHLAYAASFSPQMLARHCYYLQF 434
590 LLDRGAPCSSEGLSSVIVDHPTFRRILDTLRARIEQTTTQFMKVLVETRDYKIREGLSEA 649
                                                                                                                                                                                                                                                                                                                                    416 AGPHLAANPQTDRDG-----HVLSSQSTGSSNTEFSVDYLALICGFGAPLLARLLFYLER 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                356 EGTLPRLNALGSYTARVAGVIGAMVFSPNSALYLTEVEDSGMTEAKDGGPGPSFNRFYQF 415
                                                                                                                                                                                                                                                                                                                                                                                                320 ETPEQRYEALTQENAKQAVHVHSQLESGNSVLYLARVQKQASN--RGGGGENVYNSFFMG 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        274 A------GDCSLTIVDSVATELAVSYGLSFLEVPQFGTALLSYDKWPIFEGC 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 297 ARRNDVNSTSKPSPSGGFERRLASIMAADTALHAEVIFNTGIYEETP-TDIKEWPMFIGM 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          222 LFEAHYTSLAQALRVRDVPGLIGALERQSF---HDQYKLP-----KVYECREFPATGHRG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237 IHDCVIAPMAVALRVRNVTAVARGAAHLAFDENHEGAVLPPDITYTYFQSSSSGTTTARG 296
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Conservative 182;
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A;Acrossion: 036806
A;Molecule type: DNA
A;Molecule type: DNA
A:Mostalus: I 1128 -ALH.
A:Across references: GRCX64446; NIO:960320; PIDN:CAA45629.1; PID:960327
A:Albrecht, J.C.; Nicholas, J.; Biller, D.; Cameron, K.R.; Biesinger, B; Newman, C.;
J. Vitol. 66, 5047-5058, 1992
                                                                                                                                                        A:Title: Primary Structure of the herpesvirus saimiri genome. A:Reference number: A:7309; MUD5:9233688; PMID: 1321287 A:Confents: annotation: possible protein-coding frames A:Note: meither amino acid nor nucleotide sequence is given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, January 1992
A:Description: Frimary Structure of the herpesvirus saimiri genome
A:Reference number: A46806
                                                                       A; Gene:
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C: Keywords: DNA binding
                                                                                                                      C:Genetics:
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C:Date: 31 Dec 1992 #sequence_revision 31-Dec-1992 #text_change 16-Jul-1999
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Species: saimiriine herpesvirus 1
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                                                                                                         919 ARRPR----DPS--SVLHWIR--KD------VTSAADIETQAKALLEKTENLPELWTTAF 964
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Query Match 9.6%; Score 604, DH 1, Length 1128; Best Local Similarity 22.9%; Pred. No. 4.5e 37; Matches 275; Conservative 189, Mismatches 500, Indels 226, 865 AVKRETEEYAAINFINLPPTCIGELAQFYMANLILKYCDHSQYLINTLTSI-----ITG 751 YIVTGPYMKFLNSLHKVMF-----PNAKISALYLWHIESQKKQLPVLFGISRENMVELAN 807 DMLHGALGFILKQFHGILLFPRGMPPNSKSPNPQWFWTLLQRNQMPA-DKLFFHEE) TTTA- 864 747 DAPAGRTFDGDLARVSVEVIRDIRVKNRVVFSGNOTNI.SEAARARLVGLASAYQRQEKPV 806 601 YCCNVFWQAPCAMFLNLFYKSVLAIIQDICLPIAMTYEQDNPSIGMMPSEWLKVHY--QT 658 655 LTFDPYSGAECPITNFLVKRTHLAVVQDLAL------SQCHCVFYGQQV 697 543 VTEGTVG-SELITDIQSFLKTFRDIDNVVDSEVVKFMNCLVK-NNINFRETIKTVHHVLH 600 595 APCSSEGLSSVIVDHPTERRILDTLRARIEQTTTQFMKVLVETRDYKIREGLSEATHSMA 654 492 G-VSGQYNDLDMLGNFATF---REKEDEAVQNAESEKYTYWQLIQNVV-----EKLSTMG 535 GTMNSQYSDCDPLGNYAPYLLLRKPGDQTEAAKATMQDTYRATLEKLFIDLEQERLLDRG 476 FTGGHGDALKYVTGTFDSEIPCSLCEKHTRPVCAHTTVHRLRQRMPR-FGQATRQPIGVF 534 416 AGPHLAANPQTDRDGHVLSSQSTGSSNTEFSVDYLALICGFGAPLLARLLFYLERCDAGA 475 130 TDLRDTVDIKDLYAPFYSEDSCFMAVVVTEGFKERLYFGNLVPIIAQGLK-VQINGREAV 131 DGAVETTGAEICTRIGLEPENTILYLVVTALFKEAVFMCN-VFLHYGGLDIVHINHGDVI 189 310 PSGGFERRIASIMAADTA------LHAEVIFNTGI-YEETP-----TDIKEWPMFIGM 250 RVRNVTAVARGAAHLAFDENHEGAVLPPDITYTYFQSSSSGTTTARGARRNDVNSTSKPS 11 PTGPLGYVYACKVEDLDLEEISFLAARSTDSDLALLPLMRNL/IVEKTFTSSLAVVSGART 70 71 TGLAGAGITLKLITSHFYFSVFVFHGGKHVLFSSAAFNLIKACNAAKERFGFSKCQGPPV 130 IVP--MKMQVRLAKALLITVPKTIKIKNRIVFSN--SSMTETIQSGFIKSAT-----KKDS EGRNER******NQFQPVLRRREYDLENGGETSTRSTTVTLSEGPVSAPNPTLGQ 746 STTNANYSVPQYVGTAAASULCELCQGTCPASCIHTLFYRLKDRFPPVLGSQRRDPYVVT 491 RIPLEPVQLEMPDVNRLVPDPFNTHHRSIGEGFVYPTPFYNTGLCHLIHDCVIAPMAVAL M-----TTLLVRVSAYHREAIVFFNTDLFEPIFVGPGLDILCSDARSLFGYTNF--VPR-129 PVEPCGYTYVYPKEGFPFKEASLLGNKNVGASAMSLPLLSDLTVESNFSFNVKAVHKKID 77 HGLAYAADATQRENGEPAFSGAPKFSGGTYTLYHLALASSFSPHLLARNCYYMQFCQHQK 431 ETEEDRIKAIQDWNAMMSVHVYTHLFSTNSVLYLTKINKQTQSNKSEQN----VYNTYFMQ EGTLIPRINALGSYTARVAGVIGAMVESPNSALYLTEVEDSGMTEAKDGGPGPSFNRFYQF 415 -----DFSLQSVKCQDASAFMVIDCIAAELAMSYGLSFLEAPQDPCAVLDYTSWPIFETA 314 Gaps 371 542

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A:Molecule type: DNA
A.Residues. 1:1127 \times \text{ENS}
A:Cross-references: EMBL-AF005370: NTD:q2337967; FIDN:AAC58057 1, FTD
C:Superfamily. herpesvirus DNA binding protein
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C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 24-Nov-1999
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C;Keywords: DNA binding
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                               NSQYSDCDPLGNYAPYLILRKPGDQIEAAKATMQDTYKATLERLFIDLEQEKLLLDKGAPC 597
                                                                                         NPAYNITEYVGSAANSPY-CSLCSGQCPCVCINTLFYRLKDRFPPVLQGSRRDPYVITGI 495
                                                                                                                                                  GHG-DALKYVTGTFDSEIPCSLCEKHIRPVCAHTTVHKLKQKMPKFGQAIRQPIGVFGTM 537
                                                                                                                                                                                                                  LCEETLFEDGSPAFTGAPASSLDGSSFTLQHLAYAAAFSPNLLLARMCYYLQFCQHQKSTL 436
                                                                                                                                                                                                                                                                        AANPQTDRDGHVLSSQSTGSS--NTEESVDYLALICGEGAPLLARLLEYLERCDAGAFTG 478
                                                                                                                                                                                                                                                                                                                                        WNALQAIHIHAQLESTNSIYYVNRVARQ
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22.8%; Fred. No. 1.8e-36
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C:Species: human herpesvirus 6
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
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A; Status: preliminary; translated from GB/EMBL/DDBJ
                                    A;Title: Comparison of the complete DNA sequences of human herpesvirus 6 variants A a A;Feference number: 222732; MUID:99412319; PMID:10482554
A;Accession: T44001
                                                                                                                                          R:Isegawa, Y.; Mukai, T., Nakano, K.; Kagawa, M.; Chen, J.; Mori, Y.; Sunagawa, T.; K
J. Virol. 73, 8053-8063, 1999
                                                                                                                                                                                                                  C:Accession: T44001; T44188
                                                                                                                                                                                                                                                                                                             major DNA binding protein [imported] - human herpesvirus 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    930 HWIRKDVTSAADIETQAKALLEKTENLPELWTTAFTSTHLVKAAMN---QKPMVVLGISI 986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          818 KQFHGLLFPRGMPPNSKSPNPQWFWT-LLQRNQMPADKLTHEEITTIAAVKRF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  718 RAQVLALKNIKYKNRILESG--TSMSEHYQ-----NAFLKTANKRUNYILAGPYVKFL /68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         664 QTLW-----TNFKSFFIDKGVITGTEMKVVHAEGESDEEDVDAAFNNMYSPVKVQVRLA 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          715 VDLFNGGFISTRSITVTLSEGPVSAPNFTLGQDAFAGRTTDGD--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 657 FDPYSGAFCPITNFLVKRTHLAVVQDLALSQCHCVFYGQQVEGRNFKNQFQP--VLRRRF 714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                769 NSFHRQLF----PNLKI-SCLYLWSNFCKKKQIPCVPGVSAE-----ALNKFFSYINNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KPSYTHQGTAFEIETVKKTIQSILEDQADEDVLN-----RVVCELVKSLGAGCADLTL 1039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SKYHGAAGNNRVFQAGN---WSGLNGGKNVCPLFTFDRTRRF11ACPRGGF1CPVTG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DDIQFYLGSYGMFSENILEKLDQ-LRELVGPWTHEWAESVLK-----SGTCETDEVQF 1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SKØFEEVNMLDVVPDSYVTYAKØKLNNAILKACGQIQFYAVTIHSIFPKVQE----TCAI.
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A: Accession: 144001
A: Status: preliminary: translated from GB/EMBL/DDBJ
A: Status: preliminary: translated from GB/EMBL/DDBJ
A: Molecule type: DNA
A: Pesidues: 1-1132 < ISE>
A: Pesidues: Frain HST: pop. variant B
A: Considues: Strain HST: pop. variant B
A: Dambaugh, T R.: Stamey, F R.: Dewhurst, S.: Inoue, N.: Pellett, P.E.
T virol 73, BA040-AACS, 1999
A. Title. Human herpesvirus 6B genome sequence: coding content and comparison with hum
A: Reference number: 722734, MUID.99412318, PMID.1048253
A: A: Conscion: T44188
A: Status: preliminary: translated irom GB/EMBL/DDBJ
A: Residues: 1-1132 < DOM>
A: Pross-references: EMHL-AF157706; PIDN-AAH06339.1
A: Experimental source: strain 729; variant B
A: Experimental source: strain 729; variant B

Ś ć. Ξ Š ē Ş Ξ 4 Ş Ξ ç 3 ζ Ę Š Ş Ş Ξ A:Gene: U41 C; Superfamily: herpesvirus DNA binding protein C; Genetics Query Match 7.8%; Score 490.5; DB 2; Length 1132; Hest Local Similarity 22.9%; Pred. No. 2c 28, Matches 278; Conservative 180; Mismatches 535; Indels 273; Gaps 889 LAQFYMANLILKYCDHSQYL··INTLTS·IITG······ARRPRDPS··SVLHWIRK 934 782 PNVKISCLELWORELLNNVPKTLDIGNPERVKTFIKFAFSITNTYDEIDIIDIQPECLST 841 831 PNSK SPNPOWEWILLORNOMPADKLIHEETTT-LAAVKRFTEEYAAINFINLPPTCIGE 888 736 IKNRPENKSSKTAHNNFYFKKNV------KHKKNPLSGCISFLLFKYHDKLF---- 781 771 VKNRVVESGNCTNLSEAARAKLVGLASAYQRQEKRVDMLHGALGELLKQEHGLLEPRGMP 830 684 KCFLNTRTVKV 628 LIFAYYKVILIVLUNIAL--- IVASGHVVDKPCTGNSISKWIVQQYQSIYGTFHSSYLK 683 668 THELEKKTHLAVVOOLALSOCHCVEYGOOVEGREERNOFOPVLERKEVOLF-----N 719 571 KKDFVSTIHGLTQCTEECVS -- RCIVEMRRTQTPREQIENCLQSFNVDTTPYATAFSPF 627 526 KEIGKDOONTLS 471 COUSCICTAMVRVGIRLPAIPKNVKKEPLVMSMFSRYYAEVDILGSEG-----RKPVSEL 525 42 F CATCPOLLSYVVWNLNRMSV -720 GGFISTRSITVTLSEGPVSAPNPTLGQ--DA----PAGR----TFDGDLARVSVEVIRDIR 770 564 EAAKATMQUTYKATLEKLFIDLEQERLLDRGA------PCSSEGLSSVIVDHPTFR--- 613 504 TRPVCAHTTVHKLKORMPREGOATROPIGVEGTMNSOYSDCDPLGNYAPYLILKRPGDOT 563 454 CGFGAPILLARLLEYLERCDAGAFTGGHGDALKYVTGTFDSEI -----PCSLCEKH 503 370 SYMTO - FIRE FILLESISFONALSSITTEDYYNDNRKIIKCDSTSGKDDKFSANHLAYA 422 395 SCHTEAKDRICPGPSENRFYQFAGPHLAANPQTDRDGH-VLSSQSTGSSNTEFSVDYLALI 453 14/ 267 293 TARCARKNIDVNSTSKPSPSGGFERRLASIMAADTALHAEVIEN----TGIYEETPTDI 346 217 LSETLEYYVETSWGTTLRESNTKELLDAGLKQFTQDGEQTVKLAPHKTYL---------- 266 233 LCHLIHIXCVIAFMAVALRVRNVTAVARGAAHLAFDENHEGAVLFFDITYTYFQSSSSGTT 292 166 PCVEEQIQVOVGEYSCVKIPLYSATLFETE:-----ETISLSSCTEFIQERGFFLPA 216 116 HLOSFEYPTARKYIDIKA -LCSAYGKDADSVICHVACGNGFKEILF------AGILI 165 310 MNENDWELLRNSETHAERMAGLITNLKLHLSSHLAVLLFADNSTLYCSKLAFTDNVKQAFN 369 121 GESROGGPPVDGAVETTGAELOTRLGLEPENTTLYLVVTALFKEAVFMONVFLHYGGLDT 180 62 LAVVSGAPTTGLAGAGITELKLTTSHFYPSVFVFHGGKHVL-PSSAAPNLTRACNAARERF 120 63 V --- --- KTPITNEGGTILTKITSEMPVCEFFHGTEQLVGMAEDHGDLIRLCEQTRQKE 115 4 DENETVVSAPVSTAAWIYVEPKEKELLDVLSVLSLMERNSPVVISPLLMNLTVENDESTT 62 2 ENTOKTYTYPTGPLGYVYACKVEDLDLEELSELAARSTDSDLALLPLMRNLTVEKTETSS 61 KEWPMFIGMEGTLPRINALGSYTARVAGVIGAMVFSPNSALYLTEVE-----D 394 GISGOKISAVEKD RILDTLRAKTEOTTTOFMKVLVETRDYKI-REGLSEATHSMALTEDPYSGAFCPI 667 --VHINHGDVIRIPLEPVOLEMPDVNRLVPDPENTHHRSIGEGEVYPTPEVNTG 232 -ASNVDMEQILDCDLYKSGKYVKTTIQAKLCRLSMQCLRDFR 735 - -----LDRGKEVSQ1FDYCKKNSL1DPVTGEDTENVRS 570 FLMLVDSVV TELSFSHVAEYLDSVYD--PSQI 309 ----YNAGNAYTEIYNHLVNCSANLCEFCDGK 470 54;

Search completed: March 28, 2003, 13.39.02 Job time : 60 secs

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Post-processing: Minimum Mattch 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                 SPTREMBL_21:*

1: sp_archea:*
2: sp_bacteria:
3: sp_fungi:*
4: sp_human:*
5: sp_invertcbi
6: sp_mammal:*
7: sp_mhc:*
7: sp_mhqq::*
10: sp_phqqc:*
11: sp_virus:*
12: sp_virus:*
13: sp_vertebra
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6294
1 MENTQKTVTVPTGPLGYVYA
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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7	2793.5	44.4	1190	12	Q9QTB9	0
æ	2788	44.3	1191	12	Q9E6P0	Q9e6pt
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10	2764.5	43.9	1190	12	Q9E1G3	C
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Q92ca7		701 1		1.9	119.5	37
Q9ex54			2	1.9	120	3 6
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181 VHINHGDVIRIPLEPVQLEMPLVNRLVPDFENTHHRSIGEGEVYPIFEYNTGLCHLIHDC 240	121 GESRÖĞEPEVIĞAVETTGAELCIKLIĞLEPENITLYLEVIALEKEAVEMONVELHYĞĞILI 180 	61 SLAVVSGARTTGLAGAGITLKLITSHFYPSVFVFHGGKHVLPSSAAPNLTKACNAAKEKE 120 	1 MENTQKTYTVPTGPLGYVYACRVEDI.DLEEISFLAAPSTDSDLALLPLMRNI.TVEKTFTS 60	Query Match 73.5%; Score 4627; DB 12; Length 1194; Best Local Similarity 71.8%; Pred. No. 0; Matches 867; Conservative 143; Mismatches 178. Indels 26, Gaps	Fiam: PF00/4/; VITAL_UNA_DP; I. SEQUENCE 1194 AA; 131968 MW; EBA7F3C841965897 CRC64;	InterPro; IPR000635; Viral_DNA_bind.	EMBL; AF275348; AAG27202.1;	"COMPLETE Sequence of the Simian Varicella Virus Genome."; Submitted (MAK-Jüül) to the EMBL/CenBank/DDBT databases	Gray W.L., Starnes H.B., White M.W., Ashburn C.V., Mahalingam R.;	SEQUENCE FROM N.A.		Alphanerpesvirinde; Variceriovilus.	Viruses; dsDNA viruses, no RNA stage; Herpesviridae;	irus 7.		(TrEMBLrel. 19,	(Tremstrel. 16,	2001 (TremBLrel.	Q9EIY7; FRELIMINARY; FRT; 1194 AA.	

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                                                                                                 SCCCNIAFNFDTCNDS
                                                                                                                                             ETPINIAFNEDSCEPSHOTISNVINISCSNISCSIVP---CLKRPPEDDELFOLSCIPIK 1195
                                                                                                                                                                                                  KAEHMGFDDWLSLFDDEYLARDLEELHDÓINOTLOTPWNSDAVLEALKALNDGATVINEN 1134
                                                                                                                                                                                                                                                    KAQHMAFDDWLSLIDDEFLARDLEELHDQIIQTLETPWTVEGALEAVKIL-DEKTTAGDG 1138
                                                                                                                                                                                                                                                                                                                                                  DRIFRRELLACPROCETCPVTGPSSGNRETTLSDØVRGITVSGGAMVØLATYATVVKAVGA 1079
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Best Local Similarity
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01.JAN-1998 (TrEMBLrel. 05, Created)
01.JAN-1998 (TrEMBLrel. 05, Last sequence update)
01.DEC 2001 (TrEMBLrel. 19, Last annotation update)
Counterpart of HSV-1 gene UL29 and VZV gene 29.
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Viruses: dsDNA viruses, no PNA stage: Herpesviridae:
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GIEGTMNSTYSDODVIGNYASYGALKERND-NEADKSIMODIYRATMERIVNDI FOAKLI 596
                                                                                                                                                           YVAGNEGTEKLERVLAHTADEGEARFINGSNEETSLDYLALACGFOPQLIJAPILFYLERCD 477
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                                    GVEGTMNSQYSDCDPLGNYAPYLILEKPODQTEAAKATMQDTYPATLERLEIDLEQERLL 591
                                                                                                                                                                                                      HI.AANPQTDRDGHVLS-----SQSTGSSNTEFSVDYLALICGFGAPLLARLLFYLERCD 472
                                                                                                                                                                                                                                                                                   LPFUNAL/SYTAPVA/(VIGAMVESPNSALYLTEVEDSGMTEAKI///GP/PSFNPFYQFA//P 418
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                                                                              AGTFGGRNETDALRYLANTLESEVPCGLCTPATRPACAHTTLHRLRQRLPRFGTPVRAP1 537
                                                                                                                     AGAFTG-GHGDALKYVTGTFDSETPCSLCEKHTRPVCAHTTVHRLRQRMPRFGQATRQP1 531
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Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Schwyzer M., Vicek C., Lowery D.E., Bello L.J., Meyer G.,
                       STRAIN-JURA;
                                          SEQUENCE FROM N.A.
                                                                              Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                         STRAIN-COOPER;
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                                                                                                                                                                                                                                                                                                        Alphaherpesvirinae; Varicellovirus NCBI_TaxID=10320;
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                                                                                                    Vicek C . Pares V
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Pfam; PF00747; Viral_DNA_bp; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               479
777 RVMFSAGNANMSEAARARVLGLAGAYQKPESGGVNILSGPLGFLVKQFHRKLFPNGKPPG 836
                                                       774 RVVFSGNCTNLSEAARARLVGLASAYQRQEK-RVDMLHGALGFLLKQFHGLLFPRGMPPN 832
                                                                                                                     717 FMDLLNGGFLTTRTVTVTLAEAAVAAPNLAAAÇTFPPAKUMUGÜISKVSLEVFKEMRVKN 776
                                                                                                                                                         714 FVDLFNGGF1STRSITYTLSEGPVSAPNPTLGQDAPAGKTFDGULAKVSVEVIKD]KVKN 773
                                                                                                                                                                                                                                              657 SLALDPYSTAVCPATAFLFRRSVLAVVQDLALSQCHGIFCGQPVDGRNFRAQFQPVLRRR 716
                                                                                                                                                                                                                                                                                                                                                                   598 DAQSAAQ-LERAITDHASFRGALAAIQNTVEQATEAFVRGLVEDROFKMREALYEANHTI, 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                534 FGTMNSQYSDCDPLGNYAPYLILRKPGDQTEAAKATMQDTYRATLERLFIDLEQERILDR 593
                                                                                                                                                                                                                                                                                                                                                                                                                                 594 GAPCSSEGLSSVIVDHPTFRRILDTLRARIEQTTTQFMKVLVETRDYKIREGLSEATHSM 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421 AANPOTDRDGHVLSSQSTG-----SSNTEFSVDYLALICGFGAPLLARLLFYLERCDAG 474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unery Match 52.9%; Score 327.5; DH 12; Length 1177; Hest Local Similarity 53.5%; Pred. No. 2e 259;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wh S. L., Hsiand C. Y., Ho T. Y., Chang T.-J.;
"Identification, expression, and characterization of the pseudozabies virus DNA-binding protein gene and gene product.";
Virus Res. 56.1 '9(1978).
EMMIL UH0909, AAC64429.1:
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01 NOV 1998 (TEMBLEC): 08, Last sequence update)
01 JUN 2001 (TEMBLEC): 17, Last annotation update)
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                                                                                                                                                                                                                                  1046 LVQTAVYAAVLHALGARTQHLEPDDWRAIVDDEFLAAALAEINGRVADR-DGRWSVEAAA 1104
                                                                                                                                                                                                                                                                                   1064 MVQLAIYATVVRAVGARAQHMAFDDWLSLTDDEFLARDLEELHDQIIQTLETPWTVEGAL 1123
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Q69101;
01-NOV-1996
01-NOV-1996
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01-NOV-1996 (TrEMBLICEL 01, Last sequence update)
01-DEC-2001 (TrEMBLICEL 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro: IPR000635; Viral_DNA_bind.
Pfam; PF00747; Viral_DNA_bp; 1.
SEQUENCE 1197 AA; 128470 MW; AA3ADA75B8865BFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              simplex virus type 2 and comparison with the type 1 counterpart. ; Arch Virol 129·183-196(1993) EMBL; D10658; BAA01507.1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Herpes simplex virus (type 2).
Viruses; dsDNA viruses, no RNA stage, Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA binding protein ICP8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Nucleotide sequence of the major DNA binding protein of herpes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-93228441; PubMed-8385914; Toh Y., Tanaka S., Liu Y., Mori R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCHI_TaxID=10310;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   417
654 ALTEDRYSGARCRITNELVKKIHLAVVQDLALSQCHCVFYGQQVEGRNFRNQFQFVLRRR 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 LAVVSGARTTGLAGACITLKITTSHFYPSVFVFHGGKHVLPSSAAPNITRACNAARDRFG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 TQKTVTVPTGPLGYVY - - ACRVEDIDLEETSPLAARSTDSDLALLPLMRNLTVEKTFTSS 6.1
                                                                                          AVPTALGRLETIIGNREALHTVVNNIKQLVDREVEQLMRNLIEGRNFKFRDGLAEANHAM 654
                                                                                                                                                                        GAPOSSEGLSSVIVEHPTERKILETTRARTEQFTTQEMKVLVETKIVKTREGLSEATHSM 653
                                                                                                                                                                                                                                                                                                                                                                                                                                      VIVGRQEMDVFRYVADSGQTDVPCNLCTFFTRHACAHTTLMRLRARHPKFASAARGAIGV 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGAVGAYLARAAGLYGAMVESTNSALHLTEVDDAGPADPKDHSK-PSFYRFFLVPGTHVA 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LNALGSYTAKVAGVIGAMVESPNSALYLTEVEDSGMTEAKDGGPGPSFNREYQFAGPHLA 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VNSTSKPSPSGGFERRLASIMAADTALHAEVIFNTGIYEETPTDIKEWPMFIGMEGTLPR 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VGPAAVALRARNVDAVARAAAHLAFDENHEGAALFADITFTAFEASQG - KFQRGAR - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IAPMAVALRVRNVTAVARGAAHLAFDENHEGAVLPPDITYTYFQSSSSGTTTARGARRND 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGDAEVHRIPVYPLOMFMPDESRVIADPFNCNHRSIGENFNYPLPFFNRPLARLLFEAV 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HINHGDVIRIPLEPVQLEMPDVNRLVPDPENTHHRSIGEGEVYPTPEYNTGLCHLIHDCV 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FSDYAPRPCDLKHETTGDALCERLGLDPDRALLYLVITTEGFREAVCISNTFLHLGGMDKV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VAAVVGSGTTGLGGTAVSLKLMPSHYSPSVYVFHGGRHLAPSTQAPNLTRLCERARRHFG 124
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                                                                                                                                                                                                                                                              FGTMNSAYSDCDVLGNYAAFSALKR-ADGSENTRTIMQETYRAATERVMAELEALQYVDQ 594
                                                                                                                                                                                                                                                                                                                                           POIMNSQYSDODPLONYAPYLILAKPONOMAAKAIMQIMTYRATLERLEIDLEQEELLINE 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AFTGGHG-DALKYVTGTFDSETPCSLCEKHTRPVCAHTTVHRLRQRMPREGQATRQPIGV 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANPQLDREGHVVPGYEGRPTAPLVGGTQ-EFAGEHLAMLCGFSPALLAKMLFYLERCDGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANPOTORDGHVI. - - - - - - SSQSTCSSNTEFSVDYLALICGFGAPLLARLLFYLERCDAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FSRCQGPPVDGAVETTGAEICTRLGLEPENTILYLVVTALFKEAVFMCNVFLHYGGLDIV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --DAGNKGPAGGFEQRLASVMAGDAALALESIVSMAVFDEPPPDITTWPLLEGQETPAAR 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 47.9%; Score 3012; DB 12; Similarity 49.0%; Pred No. 6.6e-234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY:
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RESULT 6
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    Matches
                        Query Match
best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9PZ52;
01-MAY-2000 (TrEMBLre: 13, Created)
01-MAY-2000 (TrEMBLre: 13, Last sequence update)
01 JUN-2001 (TrEMBLre: 17, Last annotation update)
                                                                                                                                                                                "Identification and Transcriptional Analysis of the Marek's Disease Virus Serotype 2 Cenes Homologous to the Glycoprotein B (UL27), the ICP18.5 (UL28) and the Major DNA-binding Protein (UL29) Genes of Herpes Simplex Virus Type 1.";

J. Vet. Med. Sci. 0:0.0(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                   Alphaherpesvirinae; Marek's disease-like viruses NCBI_TaxID=10390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homolog of HSV-1 glycoprotein.
Turkey herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9PZ52
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                                                                                           SECHENCE
                                                                                                                                                                                                                                                                                                 Kato K., Jang H., Izumiya Y., Cai J., Tsushima Y., Miyazawa T.,
Kai C., Mikami T.,
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1189 LSGIPIKHGNITMEM 1203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1072 TVKSLGPRTQQLQIEDWLALLEDEYLSEEMMEFTTKALEKGHGEWSTDAALEVAHEAEAL 1131
                                                                                                          InterPro; IPR000635; Viral_DNA_bind.
Pfam; PF00747; viral_DNA_bp; 1.
                                                                                                                                                               EMBL; AB024711; BAA83753.1
                                                                                                                                                                                                                                                                                                                                                 STRAIN-HPRS24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1073 VVRAVGARAQHMAFDDWLSLTDDEFLARDLEELHDQTIQTLETPWTVEGAL----EAVKI 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  715 VMDLFNNGFLSAKTLTVALSEGAAICAPSLTAGQTAPAESSFEGDVARVTLGFPKELRVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                714 FYDLFNGGFISTRSITYTLSEG-PYSAPNPILGQDAFAGKIFDGDLARYSYEYIKDIRVK 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           655 SESEDPYTOGEOPELEGELARRSNEAVYQUELALSGOBOVERGUESVEGENGEQPVERRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VCPLETEDRTRREIIACPRGGEICPVTGESSGNREITLSG/VPGIIVSGGAMV/LAIYAT 1072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VSQLGAAGK-----VENEGDEDDHAAASEGGLAAA-AAGAAGVARKRAEHGDDPEG 1183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LDEKTTAGDGETPTNLAFNFDSCEPSHDTTSNVLNISGSNISGSTVPGLKPPPEDDELFD 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACPLLIFDRTRKFVLACPRAGFVCAASSLGGGAHEHSLCEQLRGIIAEGGAAVASSVFVA 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TENLPELWITAFISTHLVRAAMNQRPMVVLGISISKYHGAAGNNRVFQAGNWSGLNGGKN 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YMANQILRYCDHSTYFINTLTAVIAGSRRPPSVQAAAAWAPQ---GGAGLEAGARALMDS 951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YMANLILKYCDHSQYLINTLTSIITGARRPRDPSSVLHWIRKDVTSAADIETQAKALLEK 952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNÖPNPÖWFWTALÖRNÖLPARLLSKEDIETIAFIKKESLUYGAINFINLAPNNVSELAMY 894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SKSPNPQWFWTLLQRNQMPADKLTHEEITTIAAVKRFTEEYAAINFINLPPTCIGELAQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SRVLFAGASANASEAAKARVASLQSAYQKPDKRVDILLGPLGFLLKQFHAVIFPNGKPPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NRVVFSGNCTNLSEAARARLVGLASAYQRQEKRVIMLHGALGFELLKQFHGLLFPRGMPPN 832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LDAHPGAWTSMFASCNLLRPVMAARPMVVLGLSISKYYGMAGNDRVFQAGNWASLLGGKN 1011
    546;
                                                                                           1190 AA;
    Conservative 235; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                     44.4%: Score 2796.5; DB 12; Length 45.3%; Fred. No. 1.7c-216;
                                                                                           130339 MW; D9291E2EEAA7E59D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1190 AA
  396; indels
29; Caps
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6 KTVTVPTGPLGYVYACRVEDLDLEEISFLAARSTDSDLALLPLMRNLTVEKTFTSSLAVV 69

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1078 DRVRQMELDDWMEITNDAYISSLIDELNKQ-VEGGEGGWSVDAAAILAKEMVDMSKALPL 1136
                                                                                                      1079 ARAQHMAFDDWLSTTDDEFTARDI.EET.HDQTTQTTLETPWTVEGALEAVKILDEKTTAGDG 1138
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES-Gallid herpesvirus ? (seretype 2); STHAIN-HERS24;
Jang H., Cai J., Izumiya Y., Murakami Y., Mochizuki M., Song C.,
Lee Y., Kai C., Takahashi E., Mikami T.;
"The complete DNA sequence and transcription map of the unique long genome region of Marek's disease virus type 2.";
Submitted Armstood (Armstood)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000635; Viral_DNA_bind
Pfam; PF00747; Viral_DNA_bp; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AB024414; BAA82925.1; EMBL; AB049735; BAB16539.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lzumiya Y., Jang H., Ono M., Mikami T.;
"A Complete Genomic DNA Sequence of Marek's Disease Virus Type
Strain HPRS24.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES-Gallid herpesvirus 3; STRAIN-HPRS24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES Gallid herpesvirus 3; SPRAIN-HPES24;
Izumlya Y., Jang H., Ono M., Mikami T.;
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases
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Viruses; dsDNA viruses, no RNA stage, Herpesviridae;
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244 AVGLRVRNVDAIARCAAHLSFDENHEGTLLPADTAFNAFTPIESASKSQYKAGKKEGMEL
                                            246 AVALRVRNYTAVARGAAHLAFDENHFGAVLPPDTTYTTYFQSSSSGTTTAKGARRNDVNST 305
                                                                                                                                  186 GEVIRIPLEPVQLEMPOVNELVPOPENTHHESIGEGEVYET PEYNTGLCHLIHDCVIAFM
                                                                                                                                                                                                                         126 QGPPVDGAVETTGAEICTRIGLEPENTILYLVVTALFKEAVFMCNVFLHYGGIDIVHINH 185
                                                                                                                                                                               124 YSPPVATSFETTGEQICDNLGMNPQETMLYLVVTELFKEAVYLCNSYLHYGGTGVVSING
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                                                                                        VDVRRMPLYPLHLVFPDFNRVASDPFSTKPRALGEGALMPKAFYNDSLCRLLHGYVLSTA
                                                                                                                                                                                                                                                                        AGTKTTGLGSGSTTLKLVPTHYHPCVFVFHGGECIKPCTKAPNLTKACDLARGREGYS-T 123
                                                                                                                                                                                                                                                                                                                                                            KSVKITGGPIGYVYAAPTSSMPAEDLSIFAAKSNDCEDAILPLVSGLTVEADFMWNVAAV 64
                                                                                                                                                                                                                                                                                                                  SGARTTGLAGAGITLKLTTSHFYPSVFVFHGGKHVLPSSAAPNLTRACNAARERFGFSRC 125
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SEQUENCE 1191 AA; 130714 MW;
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                                                                                                                                                          GTMNSQYSD@DPIGNYAPYLILEKPGD@TEAAKA1M@DTYKATLEKHJETDLEQEKHJJDEG
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                                                                                            APCSSEGLSSVIVDHPTFRRILDTLRARIEQTTTQFMKVLVETRDYKIREGLSEATHSMA 654
                                                                                                                                    GAMTNNYCDVNALGSYAQFSTLKR--SEGEASRSVMQDTYRLTVERMMKALEKEGLLTCD
                                                                                                                                                                                                                                                FTGGHG-DALKYVTGTFDSEIPCSLCEKHTRPVCAHTTVHRLRQRMPRFGQATRQPIGVF
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44.3%; Score 2788; DB 12;
45.1%; Pred. No. 8.4e-216;
tive 237; Mismatches 395;
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Query Match
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Pram: PF00747; Viral DNA_bp; 1.
SEUHENCE: 1190 AA; 180054 MW; 8450CAF5FFF0D928 CRC64;
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01 MAR 2001 (TrEMBLIE), 16, Last sequence update)
01 DEC 2001 (TrEMBLIE), 19, Last annotation update)
UL29 single stranded DNA binding protein.
                                                                                                                                                                                                                                                                     Alonso C.L., Tulman E.R., Lu Z., Zsak L., Rock D.L., Kutish G.K., Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AF291866; AAG45767.1;
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Atonso C.L., Tulman E.F., Lu Z., Zsak L., Rock D.L., Kulish G.E.,
"The genome of turkey herposvirus.";
J. Virol. 75:971-978(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN- FC126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alphaherpesvirinae; Marek's disease-like viruses. NCHI TaxID-37108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Meleagrid herpesvirus 1 (herpesvirus of turkeys).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
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                                     y Match 44.2%; Score 2781.5; Local Similarity 44.5%; Pred. No. 2.8e hes 548; Conservative 245; Mismatches
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                                                                                                                               NVCPLFTFDRTRRFIIACPRGGFTCFVTGPSSGNRETTLSDQVRGIIVSGGAMVQLAIYA 1071
                                                                                                                                                                                                                                                           KTENLPELWTTAFTSTHLVRAAMNQRPMVVLGISISKYHGAAGNNRVFQAGNWSGLNGGK 1011
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01-MAK-2001
01-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000635; viral_DNA_bind
Pfam, PF00747; viral_DNA_bp; 1.
SEQUENCE 1190 AA; 129952 MW; A4A19239FB47DD82 CRC64;
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EMBL; AF282130; AAG30069.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alphaherpesvirinae; Marek's disease-like viruses NCBL_TaxID=37108;
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                   PHLAANPQTDRDGHVLSSQS----TGSSNTEFSVDYLALICGFGAPLLARLLFYLERCDA 473
                                                               TDRVEALSAYMGRVAGLVGAMVFSSNSVIYMTEVGEASSSDGKESGVPAPSFYRFFQIAA 412
                                                                                                    LPRLNALGSYTARVAGVIGAMVFSPNSALYLTEVEDSGMTEAKDGG-PGPSFNRFYQFAG 417
                                                                                                                                                                                     RNDVNSTSKPSPSGGFERKLASIMAADTALHAEVIFNTGIYEETPTDIKEWPMFIGMEGT 358
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                                                                                                  Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Marek's disease-like viruses. NCBI_TaxID=10390;
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Jones D., Lee L., Liu J.L., Kung H
                                         STRAIN=GA
                                                                                                                                                                 Turkey herpesvirus.
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                     MEDLINE=92237304; PubMed=1315048;
                                                               SEQUENCE FROM N.A.
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Ptum: PF00747; viral_DNA_bp: 1.
SEQUENCE: II91 AA: 130946 MW; AC04A0158B0797A3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN CA
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the tos/jun encodemes that is highly expressed in lymphoblastoid
tumors.";
                                                                                                          647 DANHILSLAVEPYASGICPVLAFLSKRTITAVVODMALSOCSIVMOGOOVEARNERTOFO 706
                                                                                                                                            648 EATHSMALTFDPYSCAFCPTTNFLVKRTHLAVVQDLALSQCHCVFYCQQVECRNFRNQPQ 707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           414 QFACPHLAANPOTDRUGHVLS --- SUSTGSSNTEESVDYLALICGEGAPLLARILEVIE 469
707 AVEKRAVEELGNAGETISKTITVILEDGOTOVPDPSKSOYDSVISNMEGDLAKATVETER 766
                                                  708 PYLKKREYDLENGGEISTRSTTYTLSEGPYSAPNETLGQDAPAGKTEDGDLAKYSVEVIR 767
                                                                                                                                                                                                                  587 GLUTCODPTNMASADANIRD/NSFIFAISTMKNIIESEASQLMRNLTEIFEYNITFGVWG 646
                                                                                                                                                                                                                                                                    589 RILIDROAPCSSEGISSVIVDHPTFERRILDTI.KARTEOTTTOFMKVI.VETRDYKTREGI-S 647
                                                                                                                                                                                                                                                                                                                                                                            529 QPHOVEGIMNSQYSDODDIGMYAPYLLLKKFGDGTEAAKAIMODTYRATLERLFIDLEGE 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    470 KUNAGAPTGGHG DALKYVTGTEDSELPCSLCEKHTRPVCAHTTVHRLKORMPREGQATE 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         409 QIAAPHESANPLYDRIXKEYSGENESKSISASQSEYSLDYLILACGECEQLLARFLEYLE 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        290 KGOSKMGKKEGSDVS GGGYERRTASLMASDATLATENVISASVYEDPIPDVNKWPIYCN 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2++ RILHGYVLSTTAVGLRVRNIDAIARGAAHIGFDENHEGTLLPADTTFTAFTPAAE---TT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175 YGGLDIVHINHGDVIRIPLEPVQLEMPDVNRLVPDPENTHHRSIGEGEVYPTPFYNTGLC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 LAKEKEGYS AYSSPAPTAFETTGOOTCEALEMDAONVMLYLVVTELEKEVTYLCNSELH 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 AAREREGESKOOGPPVDGAVETTGAETCTRLGLEPENTILYLVVTALEKEAVFMCNVELH 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                 RUDGGAKASHHULDUVKEVSSATUADMPCELCUKUSKIYCAHUTIKKLYYKLIYKFGYQMK 528
                                                                                                                                                                                                                                                                                                                       CAMCLEGAMINNYCDVNALVSYAQFSILKK - SEGEASKSVMQDTYRLTVERMMKALEKE 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEGILPRINALGSYTARVAGVIGAMVESPNSALYLTEVEDSGMTEAKD-GGPGPSFNRFY 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RGARRNOVNSTSKPSPSGGFERRIASIMAADTALHAEVIENTGIYEETPTDIKEWPMFIG 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIJHIX'VIAPMAVALRVRNVTAVAKGAAHLAFDENHEGAVLPPDITTYTYFOSSSSGTTTA 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EKTFTSSLAVVSGARTTGLAGAGITLKITTSHFYPSVFVFHGGKHVLPSSAAPNLTRACN 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 545; Conservative 236; Mismatches 400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43.1%; Score 2710; DB 12;
44.1%; Pred. No. 1.7e-209;
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                                                                                                                                                                                                                                                                                                                                                   Query Match
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MIN-2001 (TrEMRLrel 17, Last annotation update)
DNA binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Sequence of the infectious laryngotracheitis virus (SA-2 strain) unique long region UL28 to UL43."; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF168792; AAD56201.1; ...
                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00747; viral_DNA_bp; 1.
SEQUENCE 999 AA, 10H977 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-SA-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; dsDNA viruses, no RNA stage; Herpesviridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9QH63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alphaherpesvirinae; Infectious laryngotracheitis-like viruses
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142 PNALETTGEEICKSLAMDPOKTMLYLVVAEPFCEAVYVCN1YIHYGSVEILYINSKHVTR 201
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                                                131 DGAVETTGAEICTRLGLEPENTILYLVVTALFKEAVFMCNVFLHYGGLDIVHINHGDVIR 190
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                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                72 GLAGAGITLKLITTSHFYPSVFVFHGGKHVLPSSAAPNLTRACNAARERFGFSRC-QGPPV 130
                                                                                                                                                                                                22 GFIGYVYARFREEIDGKEWKILCAKSQDQPSCAIAPLIRGLTVESDFKFNVAAVIGTKSS 81
                                                                                                                                                                                                                                               13 GPLGYVYACKVEDLDLEETSELAARSTDS-DLALLPLMRNLTVEKTFTSSLAVVSGARTT 71
                                                                                               GVVGGNCTAILSPCHESTTVYIEHGGECIEFTSETENLIKICEDAREREGESSLPFNGPV 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR000635; Viral_DNA_bind.
                                                                                                                                                                                                                                                                                                Conservative 177; Mismatches 376; Indels 246; Caps
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                                                                                                                                                                                                                                                                                                                       23.0%; Score 1445, 30.5%; Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                              Length 999;
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          475 AFTGGHGDALKYVTGTFDSEIPCS-----LCEKHTRPVCAHTTVHRLRQRMPRFGQAT 527
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                                                                                                                                                                                                                                                                 -PTSIYTAVLRVLGEGMKDITAETWMAITDDKYLVNILVELREDISGS-QNGWSVATAQS 943
                                                                                                                                                                                                                                                                                                                                                                                                                           ---NGGKNVCPLFTFDRTRRFTIACPRGGFTCPVTGPSSGNRETTLSDQVRGIIVSGGAM 106
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                                                                                                                                                                                                                                                                                                                                                                       IGNSGSQSVNSALTNDPVRKFALACKRVGTILSSGQVASGFQENTIASQVRSLIDAGGS- 885
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                         PRELIMINARY;
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Best Local Similarity
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PROSITE; PS00589; PTS_HPR_SER; UNKNOWN_1.

SEQUENCE 1132 AA; 125394 MW; CF88E4F451919CBF CRC64;
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EMBL; U93872; AAB62603.1; -
InterPro; IFR002114; HPr_SerP_site.
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Ul-JAN-1998 (TrEMBLrel. 05, Last seq
Ul-MAR-2002 (TrEMBLrel. 20, Last ann
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InterPro; IPR000635; Viral_DNA_bind.
Pfam; PF00747; viral_DNA_bp; 1.
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                                               528 RQPIGVFGTMNSQYSDCDPLGNYAPYLILRKPGDCTEAAKATMQDTYRATLERLFIDLEQ 587
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                                                                                                                                                                                       372 QHGLGYLSEATVKENGASAFKGVPVSALDGSS---YTLQHLAYASSFSPHLLARMCYYLQ 428
                                                                                                                                                                                                                                    415 FAGPHLAANPQTDRDG-----HVLSSQSTGSSNTEFSVDYLALICGFGAPLLARLLFYLE 469
                                                                                                                                                                                                                                                                                  314 CETPDARLRALEVWHAEQALHIGAQLEAANSVLYLTRV--AKLPQKNQRGDANMYNSFYL 371
                                                                                                                                                                                                                                                                                                                                 355 MEGTLPRLNALGSYTARVAGVIGAMVFSPNSALYLTEVEDSGMTEAKDGGPGPSFNRFYQ 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            223 TGIAQALRVKDVSTVIQ-ASERQF--VHDQYKIPKLVQAKDFPQCASRGTDG------ 271
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RDPYVITGTAGT-YNDLEILGNEATEREEEGNPVEDAP---KYTYWQLCQNI-----" 538
                                                                                                                                       RCDAGAFTGGHG DALKYVTGTFDSETPCSLCEKHTRPVCAHTTVHRLRQRMPR-FGQAT 527
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                                                                                          FLPHHKNTNSQSYNVVDYV-GTAAPSQMCDLCUGUCPAVCINTLFYRMKDRFPPVLSNVK 487
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                                                                                                            moore P.S., Hoshoff C., Weiss R.A., Chang Y.;
"Molecular mimicry of human cytokine and cytokine response pathway
genes by KSHV.";
                                                                                                                                                                                                                                                                                                                                                                 01 MAY 1997 (TrEMBLIE). 03, Created)
01 MAY 1997 (TrEMBLIE). 03, Last sequence update)
01 MAR 2002 (TrEMBLIE). 20, Last annotation update)
                                                                                                                                                                                                                                                                                                Kaposi's sarcoma:associated herpesvirus (KSHV) (Human herpesvirus Viruses; dsDNA viruses, no PNA stage; Herpesviridae;
MEDLINE-97121480) PubMed-8962146; Russo J.J., Bohenzky R.A., Chien M.
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                                                                                                                                                                                                                                                                               Cammaherpesvirinae; Khadinovirus
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                                                SEQUENCE FROM N.A.
                                                                                             Science 274.1739-1744(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H6.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------LETEDRTRREIIACPRGGEICPVTGPSSGNRET-TLSDQVRGIIVS-GGA 1063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORDSY TVGGPYMKFLNALHKTLFP----STKTSALYLWHKIGQTTKNP11. 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TSTITGAKKPKDPSSVLHWIKKDVTSAADTETQAKALLEKTENLPELWTTAFT 965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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C., Chen J., Yan M., Maddalena
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002114; HPP_SerP_site.
InterPro; IPR002193; Mitoch_carrier:
InterPro; IPR000635; Viral_DNA_bind.
Pfam; PF00747; Viral_DNA_bp; 1
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EMBL: U75698; AAC57083.1; -.
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PROSITE; PS00589; PTS_HPR_SER; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
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656 LKMHF@1MWTNFKGACFDKGALTGGELKTVHQSMFCDLFDTDAATGGMFAPARMQVR - - -
                                                                                                                                                                                                           539
                                                                                                                                                                                                                                                                                                                                                                                                             429 FLPHHKNINSQSYNVVDYV-GTAAPSQMCDLCQGQCPAVCINILFYRMKDRFPPVLSNVK 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                372 QHGLGYLSEATVKENGASAFKGVPVSALDGSS---YTLQHLAYASSFSPHLLARMCYYLQ 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              415 FAGPHLAANPOTORDG-----HVLSSQSTGSSNTEFSVDYLALICGEGAPLLARLLEYLE 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   314 CETPUARLRALEVWHAEQALHIGAQLFAANSVLYLIKV--AKLPQKNQKGDANMYNSFYL 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 355 MEGTLPRLNALGSYTARVAGVIGAMVESPNSALYLTEVEDSCMTEAKDGGPGPSFNKFYQ 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          223 TGIAQALRVKDVSTVIQ-ASERQF--VHDQYKIPKLVQAKDFPQCASRGTDG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 APMAVALRVRNVTAVARGAAHLAFDENHEGAVLPPDITYTYF-QSSSSGTTTARGARRND 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 KKIDATTASVKLTSYH--REAIVFHNTHLFQPIFQGKGLEKLCRESRELFGFSTFVEQQH 131
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                                                                                                   SVHHILDEACNVYWDAPCPVELTLYYKSLLTVIDDICLTS--CMMYEDDNPAVGIVPSEW 655
                                                                                                                                                   EATHSMALTFDPYSGAFCPITNFLVKRIHLAVVQDLALSQCHCVFYGQ-------
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                                                -----QVEGRNER------NQEQPVLREREVDLEN------GEISTESITVTLSE 734
                                                                                                                                                                                                           EKLASMGISEGGDALRTLIVDIPSFVKVFKGIDSTVEAELLKFINCMIK-NNYNFRENIK 597
                                                                                                                                                                                                                                                         ERLLDRGAPCSSEGLSSVIVDHPTFRRILDTLRARIEQTTTQFMKVLVETRDYKIREGLS 647
                                                                                                                                                                                                                                                                                                            RDPYVITGTAGT-YNDLEILGNFATFREREEEGNPVEDAP---KYTYWQLCQNI--
                                                                                                                                                                                                                                                                                                                                                            RQPIGVEGTMNSQYSIXTDPLGNYAPYLILRKPGDQTEAAKATMQDTYRATLERLFIDLEQ 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                RCDAGAFTGGHG-DALKYVTGTFDSE1PCSLCEKHTRPVCAHTTVHRLRQRMPR-FGQAT 527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -STLMVID-SLVAELGMSYGLSFIEGPQDSCEVLNYDTWPIFEN 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        029ACFAF4C8A5ECB CRC64;
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RESULT 15
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                                 Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL: AF324455; AAK16699.1; -
InterPro; IPR002114; HPI_SCIP_SITE.
InterPro; IPR000531; TonB_boxC.
InterPro; IPR000535; Viral_DNA_bind.
Plan; PPUJ47; VIRAL_PNA_BF_1.
PROSITE; PS00589; PTS_HPR_SER; UNKNOWN_1.
                                                                                                                                                                                                                                                                  Macrae A. I. Dutia R.M. Milligan S. Rrownstein D.C., Ailen D.J., Mistrikova J., Davison A.J., Nash A.A., Stewart T.P. "Analysis of a novel strain of murine gammaherpesvirus reveals a genomic lucus important for acute pathogenesis.";

J. Virol. 75:5315-5327(2001).
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                                                                                                                                                                                                        STRAIN-MHV76;
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21232509; PubMcd-11333912;
                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-MHV76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gammaherpesvirinae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            murid herpesvirus 4.
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DNA-binding.
               PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
                                                                                                                                                                                      Davison A J
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1117 WTVEGALEAVKILDEKTTAGDGETPTNLAENFDSCEPSHDTTSNVLNTSGSN----ISGS 1172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1065 VQLATYATVVRAVGARAQHMAFDDWLSLTDDE--FLARDLEELHDQT1QTLET------P 1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1015 P-----LFTFUKIRKFIIA PRAGFICPVTGPSSGNRET-TLSDQVRGIIVSGGAM 1064
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    797 PGVSGEHLTELCNYVKASSQAFEEINVLDLVPDTLTSYAKIKLNSSILRACGQTQFYATT 856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               853 DKLTHEEITTIA-AVKRETEEYAAINFINLPPTCIGELAQFYMANLILKYCDHSQYLINT 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 735 GPVSAPNPTLGQDAPAGRTFDGDLARVSVEVIRDIRVKNRVVFSGNCTNLSEAAKARLVG 794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 795 LASAYOROEKRVDMLHCALGELLKOEHGLLEPRGMPPNSKSPNPOWEWTLL-ORNOMP-A 852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVTIVQSTLKQAVSTNGRLRPIITVPLVVNKYTGSNGNTNVFHCANLGYFSGRGVDRNLR 954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STHLVKAAMNQ------KPMVVLGISISKYHGAAGNNRVFQAGN---WSGLNCGKNVC 1014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L-----YSILTGARRPRDPSSVLHWIRKDVTSAADIETQAKALLEKTENLPELWTTAFT 965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAS--QRDSY---IVGGPYMKFLNALHKTLFP-----STKTSALYLWHKIGQTTKNPIL 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSCLSPVTQLVPAEEYP------HVLGPVGLSSPD-EYRAK------------VAGR 894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----IARAMLMVPKTIKIKNRIIFS-NSTG-AESIQAGFMK 747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANT
922 PRDPSSVLHWIRKDVTSAADIETQAKALLEKTENI.PELWTTAFTSTHLVKAAMNQRPMVV 981
                                                                                   802 VNVLDYVPTTLMAYAKQRLNNAILKLCGQTQFYATTINFLQPTILSMPSLDYPHVAG--- 858
                                                                                                                                                                                                                                             823 LLFPRGMPPNSKSPNPUWFW-TLLQRNQMP-----ADKLTHEEITTIAAVKRFTEEYAA 875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    530
                                                                                                                                                                                                                                                                                                 700 IFAPKALKIKNRIIFSNSSS--TESLSASFYKAGKAEN-----PITAGPYMHFI.TQI.HK 751
                                                                                                                                                                                                                                                                                                                                                    763 VEVTRDTRVKNRVVFSGNCTNLSEAARARLVGLASAYQRQEKRVDMLHGALGFLLKQFHG 822
                                                                                                                                                                                                                                                                                                                                                                                                           643 SNHFQNLWSNFKSIWFDKGLLTCSDMRVVHTE--TSSDMENLAADLPKQPCAI-PLSPAQ 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                              703 RNQEQPVLRRREVDLENGGETSTKSITVILSKSPVSAPNPILGQDAPAGKTFDGDLARVS 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  585 TAHVLQLQCNTNWLPPCPITHNLFTRSFFTTLQDMSFPLCVTHHTENPLNYG--TVSTWM 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     649 ATHSMALTEDPYSGAECPITNFLVKRTHLAVVQDLALSQC-----HCVFYGQQVEGKNF 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               590 LLDRGAPCSSEGLSSVIVDHPTFRRILDTLRARIEQTTTQFMKVLVETR-DYKIREGLSE 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     480 PYVVTG:IAGPHNDMEILGNEGSE--KEKDDDQ-----ENGQRYSYWQLNANL-TER 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421 NQRLASTPQGTTVPAYVTTTANTSM-CDLCGGDLPAVCLHTLFFRURDRFPQVLATQKRD 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   473 AG--AFTGGHGDALKYVTGTFDSEIPCSLCEKHTPPVCAHTTVHPLRQRMPR-PGQATFQ 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         363 GLGHL--NVQTRDENNTVVFPGVPDSCMNGSQYTVHHLAYAASMSPHILAKLCYYLQMCQ 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          417 G-PHIAANPOTDRDGHVLSSOSTGSS---NTEFSVDYLALICGFGAPLLARLLFYLERCD 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                304 PEGRIKALQEWNAKMAIHVHAQVLSANSVLYVTKVGQSA-GKAVGGKQDDMFLSRYYMQH 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    360 P--RLNALGSYTARVAGVIGAMVFSPNSALYLTEVEDSGMTEAKDGGPGPSF-NRFYQFA 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 209 YYTNVAQAVRIRDVTGLIEALQERAVTEQYKTAKLASLKTY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 VIAPMAVALRVRNVTAVARGAAHLAFDENHEGAV.PPDITYTYFQSSSSGTTTARGARRN 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 VHINHGDVIRIPLEPVQLEMPDVNRLVPDPENTHHRSIGEGEVYPTPFYNTGLCHLIHDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 NVK----APCQKIMEESLTVKPT--KYENHAIVEHNSNKIPPIEHGRGLEQLCEATRIME 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
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                                                                                                                                      QLFP-----TTKTGAYYIWQTFMSSKKI.PQAGSTNAKKLS-EF1SYLMTSSI.AHDE--- 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEEIGVTASTPA-CQLITDVDSFLTVFKKIDAIVDEETIRFNDGLVRNNINYK--ESVKS 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIGVFGTMNSQYSDCDPLGNYAPYLLLKKPGDQTEAAKATMQDTYKATLEKLFIDLEQER 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GFSRCQGPPVDGAVETTGAEICTRLGLEPENTILYLVVTALFKEAVFMCNVFLHYGGLDI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLAVVSGARTTGLAGAGITLKLTTSHFYPSVFVFHGGKHVLPSSAAPNLTRACNAARERF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      METTNVCSQAPLGPAGYIYYQLVDDFPLEEASLLSTNFTSAKACLLPLVTGLTVEPGFNF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    *****PAENCGAGNLEYAVIDAAVSELAVSHGLAFLEAPQEESPIQNYVQWPMF***SEDAT 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DVNSTSKPSPSGGFERRLASIMAADTALHAEVIFNTGIYEETP-TDIKEWPMFIGMEGTL 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VTINNKLCFKVPLHDTRFLSSD--QLL-------PFYDENVSRIMYES 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GFSSFKPDASKGQWKSS-----THLPQNPEKYIGWVVVAESFKERLICGELAMLSAPMKT 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          356 356 S -> G.
1103 AA; 123272 MW; 056359648CE27CO3 CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative 194; Mismatches 535; Indels 199; Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.4%; Score 652.5; DB 12; Length 1103, 23.9%; Pred. No. 3.1e-43;
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OF HSS PUPP-- ODLIFYMOMTRIOSATVIOSSCRED---------TRR 1024

OY "H2 IGISISKYHGAAGNNRVEQAGNWSGLNGKNNCCPLETEDR------TRR 1024

ID 900 IPMMVNKYSGSNGNNSIFOSGN MGYPMGRGV-----DRKLLPDIPRNRKHVNTSMRR 952

OY 1025 FILACPRGGFICPVTGPSGNKETTLSDOVR----GILVSGGAMVQLALYATVVRAVGAR 1080

OY 1025 FILACPRGFICPVTGPSGNKETTLSDOVR----GILVSGGAMVQLALYATVVRAVGAR 1080

OY 1025 FILACPRGFICPVTGPSGNKETTLSDOVR----GILVSGGAMVQLALYATVVRAVGAR 1080

OY 1025 FILACPRGFICPVTGPSGNKETTLSDOVR----GILVSGGAMVQLALYATVVRAVGAR 1080

OY 1025 FILACPRGFICPVTGPSGNKETTLSDOVR-----GILVSGGAMVQLALYATVVRAVGAR 1080

OY 1025 FILACPRGFICPVTGPSGNKETTLSDOVR-----GILVSGGAMVQLALYATVVRAVGAR 1080

OY 1025 FILACPRGFICPVTGPSGNKETTLSDIASGNAEPE-NLVLELVKCLGHE 1009

OY 1025 FILACPRGFICPVTGPSGNKETTLDIASGNAEPE-NLVLLEVKCLGHE 1009

OY 1025 FILACPRGFICPVTGPSGNKETTLDIASGNAEPE-NLVLLEVKCLGHE 1009

OY 1025 FILACPRGFICPVTGPSGNKETTLLDIASGNAEPE-NLVLLEVKCLGHE 1009

OY 1025 FILACPRGFICPVTGPSGNKETTLLDIASGNAEPE-NLVLLEVKCLGHE 1009

OY 1025 FILACPRGFICPVTGPSGNKETTLLDIASGNAEPE-NLVLLEVKCLGHE 1009

OY 1025 FILACPRGFICPVTGPSGNKETTLLASGNAPPERSTANGAR 1138

OY 1025 FILACPRGFICPVTGPSGNKETTLLASGNAPPERSTANGAR 1009

OY 1025 FILACPRGFICPVTGPSGNKETTLSGNAPPERSTANGAR 1009

OY 1025 FILACPRGFICPVTGPSGNAPPERSTANGAR 1009

OY 1025 FILACPRGFICPVTGPSGNAPPERSTANGAR 1009

OY 1025 FILACPRGFICPVTGPSGNAPPERSTANGAR 1009

OY 1025 FILACPRGFICPVTGPS
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Result
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            btal number of hits satisfying chosen parameters:
    333000055433010111111111008
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Maximum Match 100%
Listing first 45 summaries
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AFC. MOUSE
AFC. MOUSE
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P2P_LACPA
BCSC_PSEFL
PC16_HUMAN
ERY2_SACER
                                                                                                                                    DNBI_HSVSA

INBI_HSV6Z

DNBI_HSV7J

DNBI_HSV7J

DNBI_SCMVC

DNBI_HCMVT2

DNBI_HCMVT2

DNBI_HCMVS

2295_HUMAN
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DNBI_HSV11
DNBI_HSV11
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IF2C_EUGGR
 TEGU_EBV
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                                                                                  P18461 gallus gall

USxeký euglena gra

Q09417 caenorhabdi

P11654 rattus norv

P12785 rattus norv
                                                                                                                                                       P52339 human herpe
P13215 simian cyto
P17147 human cytom
Q9wrl7 herpesvirus
                                                                                                                                                                                                      P36384 herpes simp
P12639 bovine herp
Q03444 equine herp
P03227 epstein bar
P24910 herpesvirus
P52338 human herpe
                                      P58937
          ú96jqú homo sapien
Q03132 saccharopol
P15558 pseudomonas
                                                                Q61789 mus musculu
Q61315 mus musculu
                                                                                                                                   P30672 murine cyto
Q9ulj3 homo sapien
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P17470
P04296
                                                        Q60106 xanthomonas
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P17469 herpes simp
P89452 herpes simp
                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                                                                                                              P09246 varicella-z
epstein-bar
                                    lactobacill pseudomonas
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herpes simp
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DNBI_HSVEB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Telford E.A.R., Watson M.S., McBride K., Davison A.J., "The DNA sequence of equine herpesvirus-1."; Virology 189:304 316(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA-binding; DNA replication; Zinc-finger; Nuclear protein ZN_FING 503 516 C2HC-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M86664; AAB02466.1; -. PIR; E36798; DNBEC4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DHC-1992 (Rel. 24, Created)
01-DHC-1992 (Rel. 24, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- SUBCELLULAR LOCATION: Nuclear (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-92295566; PubMed-1318606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alphaherpesvirinae; Varicellovirus.
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                                          359 LPRINALGSYTARVAGVIGAMVESPNSALYLTEVEDSGMTEAKDGGPGPSENRFYQFAGP 418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: SINGLE-STRAND DNA-FINDING PROTEIN REQUIRED FOR
                                                                                                                                                                         VLGPAAVALRVRNLDGVARGAAHLALDENHEGSVLPQDVTFTLFDSTQGNAGKGSGRAQF
                                                                                                                                                                                                               VIAPMAVALRVRNVTAVARGAAHLAFDENHEGAVLPPDITYTYFQSS--SSGTTTARGAR
                                                                                                                                                                                                                                                            VTIDGQDAMKIPIYPVQLYMPDVNRLASEPFNAKHRSIGDFFVYSPPFFNSDLCFLLHGY
                                                                                                                                                                                                                                                                                                                                                GFSAFSSPPVENAVETSGEE1CASLNLSPETTALYLVVTESFKEMVYVCNTFLHYGGTST
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                                                                                     QGD-GSGSKNSASSGIERRLASVMAADTALSVDSIMGAGIYUIELPSVEDWPVLSSGDDT
                                                                                                                              RNDVNSTSKPSPSGGFERRLASIMAADTALHAEVIENTGIYEETPTDIKEWPMFIGMEGT 358
                                                                                                                                                                                                                                                                                                     VHINHGDVIRIPLEPVQLEMPDVNRLVPDPENTHHRSIGEGFVYPTPFYNTGLCHLIHDC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MESAPKTVSI.PVSPI.GYVYARQKASI.QTGTVSI.TAARSVDSDI.AVI.PVTRGI.TVEQTFTT 6.0
-ESLEALGAYAARLSGLVGAMVFSANSVLYMTEVDDGGPADGKDGS-NPSYHRFYLLAAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.5%; Score 3620.5; DB 1; Length 1209; 57.1%; Pred. No. 7.1e-272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119981 MW; 1A728FB04484FE95 CRC64;
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P17470;
P17470;
01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
16-OCT-2001 (Rel 40, Last annotation update)
16-OCT-2001 (Rel 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSV1K
                                                                                                                           Herpes simplex virus (type 1 / strain KOS).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
                                                                                                                                                                                                                                                                                Major DNA-binding protein (Infected cell protein DBP OR UL29 OR ICP8.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239 LLFEAVVGPAAVALRCRNVDAVARAAAHLAFDENHEGAALPADITFTAFEASQG--KTPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236 LIHDCVIAPMAVALRVRNVTAVAKGAAHLAFDENHEGAVLPPDITYTYFQSSSSGTTTAR 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 ARRHFGFSDYTPRPGDLKHETTGEALCERLGLDPDRALLYLVVTEGFKEAVCINNTFLHL 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 METKPKTATTIKVPPGPLGYVYARACPSEGIEL - LALLSARSGDADVAVAPLVVGLTVE
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                                        RQPIGVFGTMNSQYSDCDPLGNYAPYLILRKPGDQTEAAKATMQDTYRATLERLFIDLEQ 587
                                                                                                                                                                                                                                                                                                                                                                                 AGPHLAANPQTDRDGHVL-----SSQSTGSSNTEFSVDYLALICGFGAPLLARLLFYL 468
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                                                                                                                                 ERCDGGVIVGRQEMDVFRYVADSNQTDVPCNLCTFDTRHACVHTTLMRLRARHPKFASAA 529
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                                                                                                                                                                                                                 ERCDAGAFTGGHG-DALKYVTGTFDSETPCSLCEKHTRPVCAHTTVHRLRQRMPRFGQAT 527
                                                                                                                                                                                                                                                                                                 PGTHVAANPQVDREGHVVPGFEGRPTAPLVGGTQ-EFAGEHLAMLCGFSPALLAKMLFYL
IPR000635; Viral_DNA_bind.
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type 1 containing the genes for DNA polymerase and the major DNA binding protein.";
Nucleic Acids Res. 13-8143-8163(1985).

Hammerschmidt W., Conraths F., Mankertz J., Buhk H.-J., Pauli G.,

PubMed-2457278;

MEDITINE=88306232;

SEQUENCE OF 1062-1196 FROM N.A.

Ludwig H.,

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                                                                                                                                                                               McGeoch D.J., Dalrymple M.A., Davison A.J., Dolan A., Frame M.C., McNab D., Perry L.J., Scott J.E., Taylor P.;
                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDILINE-88274327; PubMed-2839594;
                                                                                                                                                                                                                                                                                                                                           Herpes simplex virus (type 1 / strain 17).
Viruses: dsDNA viruses, no PNA stage: Herpesviridae;
                     Quinn J.P., McGeoch D.J
                                                                                                                               "The complete DNA sequence of the long unique region herpes simplex virus type 1.";
                                                                                                                                                                                                                                                                                                                                                                                           Major DNA binding protein (infected cell protein 8) (ICP DBP OR UL29 OR ICP8.
                                                                                                                                                                                                                                                                                                                                                                                                                                      20 MAR 1987 (Rel. 04. Created)
20 MAR 1987 (Rel. 04. Last sequence update)
16 CCT 2001 (Rel. 40. Last annotation update
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                                             MEDITINE-86067223; PubMed-2999714;
                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                        Alphaherpesvirinae: Simplexvirus.
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                                                                                                                Gen. Virol. 69:1531 1574(1988)
sequence of the region in the genome of herpes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA-binding; DNA replication; Zinc-finger; Nuclear protein 
ZN_FING 499 512 C2HC-TYPE.
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PIR; B30085; B30085.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to licensewisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between the Swiss Institute of Bioinformatics and the EMBH: outstat
the European Bioinformatics Institute. There are no restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                 356 EGTLPRLNALGSYTARVAGVIGAMVESPNSALYLTEVEDSGMTEAKDEGPGPSENREYQE 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPLICATION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPARTMENTS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBTELLULAR LIGATIONS NUTLEAR IN THE ABSENCE OF INA REPLICATION
DTAAARANAVGAYLARAAGLVGAMVESTNSALHLTEVDDAGDADDKDHSK-PSFYRFELV 410
                                                                                                                                                                                 LIHDOVIAPMAVALRVRNVTAVARGAAHLAFDENHEGAVLFFDITYTYFQSSSSGTTTAR 295
                                                                                                                                                                                                                                                            GGLDIVHINHGDVIRIPLEPVQLEMEDVNRLVPDPENTHHPSIGEGEVYPTPFYNTGLCH 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                METKPKTATTIKVPPGPLGYVYARACPSEGIEL -- LALLSARSGDSDVAVAPLVVGLTVE 58
                                                                                                                  GARRNDVNSTSKPSPSGGFERRLASIMAADTALHAEVIENTGIYEETPTDIKEWPMFIGM 355
                                                                                                                                                                                                                                       GGSDKVTIGGAEVHRIPVYPLQLEMPDESRVIAEPENANHRSIGEKETYPLPEENRPLNR 238
                                                                                                                                                                                                                                                                                                                    ARRHEGESDYTPRPGDLKHETTGEALCERLGLDPDRALLYLVVTEGEKEAVCINNTELHL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                       KTFTSSLAVVSGARTTGLAGAGITLKLTTSHFYPSVFVFHGGKHVLPSSAAPNLTRACNA 115
                                                                                                                                                          LLFEAVVGPAAVALRCRNVDAVARAAAHLAFDENHEGAALPADITFTAFEASQG--KTPR 296
                                                                                                                                                                                                                                                                                                                                                          AKEKEGESKOOGEEEVOGAVETTGAETOTRIGIEPENTTLYLVVTALEKEAVEMONVELHY 175
                                                                                                                                                                                                                                                                                                                                                                                                 SGFEANVAVVVGSRTTGLGGTAVSLKLTPSHYSSSVYVFHGGRHLDPSIQAPNLTRLCER 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1196 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative 199; Mismatches 367; Indels 48;
                                                                           -DGGGKGAAGGFEQRLASVMAGDAALALESIVSMAVFDEPPTDISAWPLFEGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48.4%, Score 3049, DB 1;
49.8%; Pred. No. 1.3e-227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            license agreement (See http://www
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128349 MW:
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         SEQUENCE FROM N.A
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Pfam; PF00747; Viral_DNA_bp; 1.
DNA-binding; DNA replication; Zinc-f
ZN_FING 499 512 C2HC-TY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- SUBCELLULAR LOCATION: NUCLEAR. IN THE ABSENCE OF DNA REPLICATION. FOUND IN THE NUCLEAR FRAMEWORK-ASSOCIATED STRUCTURES (PREREPLICATIVE SITES); AS VIRAL DNA REPLICATION PROCEEDS, IT MIGRATES TO GLOBULAR INTRANUCLEAR STRUCTURES (PEPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Conservation of a gene cluster including glycoprotein B in bovine herpesvirus type 2 (BHV-2) and herpes simplex virus type 1 (HSV-1)."; Virology 165.388-405(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SIMILARITY: BELONGS TO THE HERPESVIRUSES DNA-BINDING PROTEIN
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                                                               EATHSMALTEDPYSGAFCPITNFLYKRTHLAVVQDLALSQCHCVFYGQQVEGRNFKNQFQ 707
                                                                                                                                                                                          ERLLDRGAPCSSEGLSSVIVDHFTFRRILDTLKARIEQTTTQFMKVLVETRDYKIREGLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PGTHVAANPQVDREGHVVPGFEGRPTAPLVGGTQ-EFAGEHLAMLCGFSPALLAKMLFYL 469
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{\tt EANHAMSLTLDPYACGPCPLLQLLGRRSNLAVYQDLALSQCHGVFAGQSVEGRNFRNQFQ}
                                                                                                                                     LQYVDQAVPTAMGRLETIITNREALHTVVNNVRQVVDREVEQLMRNLVEGRNFKFRDGLG
                                                                                                                                                                                                                                                                    RGAIGVFGTMNSMYSDCDVLGNYAAFSALKR-ADGSETARTIMQETYRAATERVMAELET 588
                                                                                                                                                                                                                                                                                                              ROPIGVEGTMNSOYSDCDPLGNYAPYLILRKPGDQTEAAKATMQDFYRAFILFIDILEQ
                                                                                                                                                                                                                                                                                                                                                                                                      ERCDGAVIVGROEMDVFRYVADSNOTDVPCNLCTFDTFHACVHTTIMFLFARHPKFASAA
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49.8%; Pred. No. 1
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                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss lustitute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01 NOV 1997 (Rel. 35, Created)
01 NOV 1997 (Rel. 35, Last sequence update)
16 (XT: 2001 (Rel. 40, Last annotation update)
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DNA binding: DNA replication; Zinc tinger; Nuclear protein
                         InterPro: IPR000635; Viral_DNA_bind. Plan; PF00747; Viral_DNA_bp; 1.
                                                                             EMBL; Z86099; CAB06754.1;
                                                                                                                            or send an email to license isb-sib.ch).
                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (FEB 1997) to the EMBL/Genhamk/DDBJ databases. I FUNCTION: SINGLE STRAND DNA BINDING PROTEIN REQUIRED FOR DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           V or local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOBI Tax [D-10315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alphaherpesvirinae: Simplexvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Herpes simplex virus (type 2 / strain HG52).
Viruses, dsDNA viruses, no RNA stage: Herpesviridae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DHP OR ULZ9 OR ICPB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Major DNA: binding protein (Infected cell protein 8) (ICP 8 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HZASH THNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1174 FHGDDPFG EGPPDKKGDLTLDM 1195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1006 LMGGKNACPLLIFDRTRKFYLACPRAGFYCAASSLGGGAHESSLCEQLRGIISEGGAAVA 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P89452;
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                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCALION: Nuclear (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                  REPLICATION.
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953 TENLPELWITAFISTHLVRAAMNQPPMVVLGISISKYHGAAGNNRVFQAGNWSGLNGGKN 101:
                                                        895 YMANQILRYCDHSTYFINTLTAVIAGSRRPPSVQAAAAWAPQ---GGAGLEAGARALMDS 951
                                                                                                           893 YMANLILKYCDHSQYLINTLITSIITGARRPRDPSSYLHWIRKDYTSAADIETOAKALLEK 952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 TIGDAEVHRIPVYPLQMFMPDFSRVIADPFNCNHKSIGENFNYPLFFFNKPLAKLLFEAV 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 TQKTVTVPTGPLGYYY--ACRVEDLDLEEISFLAARSTDSDLALLPLMRNLIVEKTFTSS 61
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                                                                                                                                                                       SNOPNPOWFWIALQRNQLPARLLSREDIETIAFIKRESLDYGAINFINLAPNNVSELAMY 894
                                                                                                                                                                                                                                SKSPNPQWFWTLLQRNQMPADKLTHEELITTIAAVKRFTEEYAAINFINLPPTCIGELAGF 892
                                                                                                                                                                                                                                                                                         SRVLFAGASANASEAAKARVASLQSAYQKPDKRVD11.1.GP1.GF1.1.KQFHAV1FPNGKPPG
                                                                                                                                                                                                                                                                                                                                           NRVVESGNCTNLSEAARARLVGLASAYQRQEKRVDMLHGAL/FEILKQFHGLLFPPGMPPN 832
                                                                                                                                                                                                                                                                                                                                                                                                    VMDLFNNGFLSAKTLTVALSEGAATCAPSLTAGQTAPAESSFEGDVARVTLGFPKELRVK
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                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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1: FUNCTION: SINGLE-STRAND DNA-BINDING PROTEIN REQUIRED FOR DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA-binding; DNA replication; Zinc-finger; Nuclear protein.
ZN_FINC 499 512 C2HC-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ol-JUN-1994 (Rel. 29, Created)
Ol-JUN-1994 (Rel. 29, Last sequence update)
16-007-2001 (Rel. 40, Last annotation update)
Major DNA-binding protein (Infected cell protein 8) (ICP 8 protein).
DBP OR UL29 OR ICP8.
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000635; Viral_DNA_bind.
Pfam; PF00747; viral_DNA_bp; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Herpes simplex virus (type 2).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1132 VSQLGAAGE------VFNFGDFGDEDDHAASFGGLAAA--AGAAGVARKRAFHGDDPFG 1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: Nuclear (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID-10310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alphaherpesvirinae; Simplexvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P36384;
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185 TIGDAEVHRIPVYPLOMEMPDESRVIADPENCNHRSIGENENYPLPFENRPLARLLFEAV 244
                                   182 HINHGDVIRIPLEPVQLEMPDVNRLVPDPENTHHRSIGEGEVYPTPFYNTGLCHLIHDCV 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1073 VYRAVGARAQHMAFDDWLSLTDDEFLARDLEELHDQIIQTLETPWTVEGAL----EAVKI 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1012 ACPLLIEDRTRKFVLACPRAGFVCAASSLGGGAHEHSLCEQLRGIIAEGGAAVASSVFVA 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1013 VCPLFTFDRTRRFIIACPRGGFICPVTGPSSGNRETTLSDQVRGIIVSGGAMVQLAIYAT 1072
                                                                                                                        122 FSRCQGPPVDGAVETTGAEICTRIGLEPENTILYLVVTALFKEAVFMCNVFLHYGGLDIV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 952 DAHPGAWTSMEASCNILEPPMAARPMVVLGLSTSKYYGMAGNDRVFQAGNWASILGGKN 1011
                                                                                                                                                                                                                                                                                                                                               y Match
Jocal Similarity 49.0%; Pred No. 7.9e-
hes 595; Conservation 213.
                                                                                                                                                                 65 VAAVVGSGTTGLGGTAVSLKLMPSHYSPSVYVFHGGRHLAPSTQAPNLTRLCERARRHFG
                                                                                                                                                                                                         62 LAVVSGARTTGLAGACITIKITTSHFYPSVFVFHGGKHVLPSSAAPNLTRACNAARERFG 121
                                                                                                                                                                                                                                                 7 TTTTTVKVPPGPMGYVYGRACPAEGLEL--LSLLSARSGDADVAVAPLIVGLTVESGFRAN 64
                                                                                                                                                                                                                                                                                              4 TQKTVTVPTGPLGYVY--ACRVEDLDLEEISFLAARSTDSDLALLPLMRNLTVEKTFTSS 61
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                                                                                  FSDYAPRPCDLKHETTGDALCERLGLDPDRALLYLVITEGFREAVCISNTFLHLGGMDKV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A48350; A48350.
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                                                                                                                                                                                                                                                                                                                                                                                                                       1169 1197 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL). 1197 AA; 128412 MW; C1576BB5B8865BFB CRC64;
                                                                                                                                                                                                                                                                                                                                      47.9%, Score 3013; DB 1; Length 1 nilarity 49.0%; Pred No. 7.9c 225, Conservative 213; Mismatches 367, Indels
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1184 -EGPPEKK-DLTLDM 1196
                                            1189 LSGIPIKHGNITMEM 1203
                                                                                     1132 VSQLGAAGE-----VFNFGDFGDADDHAASFGGLAAA-AAGAAGVARKRAFHGDDPFG 1183
                                                                                                                                          1129 LDEKTTAGDGETPTNLAFNFDSCEPSHDTTSNVLNISGSNISGSTVPGLKRPPEDDELFD 1188
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                                                                                                                                                                                                 1072 TYKSLGPRTQQLQIEDWLALLEDEYLSEEMMEFTTRALERGHGEWSTDAALEVAHEAEAL 1131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          714 FVDLFNGGFISTRSITVTLSEG-PVSAPNPTLGQDAPAGRTFDGDLARVSVEVIRDIRVK 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           654 ALTEDPYSGAECPITNELVKRTHLAVVQULALSQCHCVFYGQQVEGRNERNQEQPVLRRR 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  595 AVPTALGRLETIIGNREALHTVVNNIKQLVDREVEQLMRNLIEGRNFKFRDGLAEANHAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 594 GAPCSSEGLSSVIVDHPTFRRILDTLRARIEQTTTQFMKVLVETRDYKIREGLSEATHSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     536 FGTMNSAYSDCDVLGNYAAFSALKR ADGSENTRTIMQETYRAATERVMAELEALQYVDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       534 FGTMNSQYSDCDPLGNYAPYLILRKPGDQTEAAKATMQDTYFATLERLFIDLEQERLLDR 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        475 AFTGGHG-DALKYYTGTFDSEIPCSLCEKHTRPVCAHTTVHRLRQRMPREGQATKQPIGV 533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YMANQILRYCDHSTYFINTLTAVIAGSRRPPSVQAAAAWAPQ---GGAGLEAGARALMDS 951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNQPNPQWFWTALQRNQLPARLLSREDIETIAFIKRESLDYGAINFINLAPNNVSELAMY 894
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DNBI_HSVB2 ID DNBI_HSVB2

STANDARD;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouvry Match 46.6%; Score 2933; DB 1; Best Lacal Similarity 48.7%; Pred. No. 1.2e-218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01 OCT 1989
01 AUG 1990
16 OCT 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS PROT entry is expyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               *Common epitopes of alycoprotein B map within the major DNA-binding proteins of bovine herpesvirus type 2 (BHY-2) and herpes simplex virus type 1 (BSV 1)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovine herpesvirus type 2 (strain BMV) (Bovine mammillitis virus).
Viruses; dsiNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA binding: DNA replication; Zinc-tinger: Nuclear protein ZN FING 495 508 C2HC-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1058-1186 FROM N.A. MEDILINE-88306232; PubMed-2457278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              herpesvirus type 2 (BHV 2)
Virology 165:388-405(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DBP OR UL29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Virology 165:406 418(1988)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hammerschmidt W., Conraths F., Mankertz J., Buhk H.-J., Pauli G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Conservation of a gene cluster including glycoprotein B in bovine herpesvirus type 2 (BHV 2) and herpes simplex virus type 1 (BSV-1).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hammersehmidt W., Conraths F., Mankertz J., Pauli G., Ludwig H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDITINE 88 106231; PubMed-2841793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pram; PF00747; viral_DNA_bp; l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro: IPR000635; Viral DNA_bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to licensewish-sib.ch).
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                                                                                                                                                                                                                                 121 VOPGESSEKPKPCEAEGETTGEALCEHLGLNPNESLLYMVIAEGEKEAVYISNTILHMGG 180
                                                                                                                                                                                                                                                                             118 ERFGESROOGEPVEGAVELIGAETOTRIGLEEENTTIJTVVTALEKEAVEMONVELHYGG 177
                                                                                                                                                                                                                                                                                                                              61 FDVNVAVVVGSRTTGVGGTGVSLKLMPSHYAPSAYVFHGGRHLAPSSAAPNLSLLCDRAP 120
                                                                                                                                                                                                                                                                                                                                                                        SH FTSSLAVVSGARTTGLAGAGITLKITTSHFYPSVFVFHGGKHVLPSSAAPNLTRACNAAR 117
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AUG 1990 (Rel. 15, Last sequence update)
orf 2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                       1 MENKOKTATTVKVSPGPLGYVYARRI.PPEGLTELALLSARSADSDTAVLPL.LAGLTVESG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MENTQKTVT VPTGPLGYVYAGRVEDLDLEEISFLAARSTDSDLALLPLMRNLTVEKT 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: SINGLE STRAND DNA BINDING PROTEIN REQUIRED FOR DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SHHCELLULAR LOCATION: Nuclear (Probable). SIMILARITY: HELONGS TO THE HERPESVIRUSES DNA-HINDING PROTEIN
                                            FGAAVGPAAVALRARNVDAVARAAAHLAFDENHEGAALPADITFTAFDPTGS-----KAG 295
                                                                                                                                                                 LDIVHINHGDVIRIPLFPVQLFMPDVNRLVPDPFNTHHRSIGEGFVYPTPFYNTGLCHLI 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPLICATION.
RKNOVNSTSKPSSCSFERKLASIMAADTALHAEVIENTGIYEETPTDIKEWPMFIGMEG 357
                                                                                                                                      VGTVTTAGEEVRRIPTYPLOMEMPDYCHAVADPENDRHRATGEYFAYPLPFENAKLASLL 240
                                                                                        HIXIVIAPMAVALRVRNVTAVARGAAHLAFDENHEGAVLPPDIIYTYFOSSSSGTTTARGA 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 585; Conservative 188; Mismatches 373; Indels 56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1186;
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DNBI_HSVEI STANDARD: PRT; 375 AA. 003444; 01-FEB-1994 (Rel. 28, Created) 01-FEB-994 (Rel. 28, Last sequence update) 16 OCT-2001 (Rel. 40, Last annotation update)

Major DNA-binding protein (Fragment). 31.

DNBI_HSVE1

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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           472 DAGAFTG-GHGDALKYYTGTFDSELPOSLOEKHTRPVCAHTTVHRLRQRMPRFGQATRQP 540
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                                                                                                                                                                                                                                                                                                                                                                                                                         GKNACPLLIFDRTRKFVIACPRAGFVCAAVSAGSGAHESSI.CEQI.RAIIAECGATVASDV 1064
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMYYMANQILKYCDHSTYF1NTLTALIAGSRRPPNAQAAAAWAPRGGT---ELEAQARSV 944
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                                                                                                                                                                                                                                                       --AGDGETPTNLAFNFDS---
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RESULT 10
DNB1_EBV
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DWH1_ERV STANDARD; FP03227; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last seq 16-OCT-2001 (Rel. 40, Last annotation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bell C W , Whalley J.M.;
"Herpesvirus ICP18.5 and DNA-binding protein genes are conserved in equine herpesvirus-1.";
Virus Cenes 7:219-228(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                             1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA-binding; DNA replication; Nuclear protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=94106109; PubMed=8279122;
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                                                                                                                                                                                                                 353 PDDILEDMGAPPEKKSGLIFDM 374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Nuclear (Probable)
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                                                                                                                                                                                                                                                            EDDELFDLSGIPIKHGNITMEM 1203
                                                                                                                                                                                                                                                                                                    NMEAQTTAGAVAAGEG----AFDFGACVGDTPQQSTSA----FNGGLAMAAAPAGQKRSL
                                                                                                                                                                                                                                                                                                                                              ILDEKTTAG---DGETPTNLAFNFDSC---EPSHDTTSNVLNISGSNISGSTVPGLKRPP 118
                                                                                                                                                                                                                                                                                                                                                                                         {\tt AVFAAVLHALGARTQHLAVDDWIGLVDDEFLAASLDALNATVVDQF: GEWSVEAAQELVK}
                                                                                                                                                                                                                                                                                                                                                                                                                                   AIYATVVRAVGARAQHMAFOGWLSLTDDEFLARDLEELHDQIIQTLETPWTVEGALEAVK 1127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NGGKNVCPLFTFDRTRPFTIACPRGGFICPVTGPSSGNRETTLSDQVRGIIVSGGAMVQL 1067
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         Last sequence update)
Last annotation update)
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Pfam; PF00747; viral_DNA_bp; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Epstein-barr virus (strain By5-8) (Human herpesvirus 4). Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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PIR; S33057; S33057.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www isb-sib-ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: Nuclear (Probable)
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                            371 LQEGTWDPCRRPCFSGWGGPDVTG-----TNGPGN--YAVEHLVYAASFSPNLLARYAY
                                                                                                                                                                361
                                                                                                                                                                                                                                                                                                                                              247
                                                                                                                                                                                                                                                                                                                                                                                         182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73 LAGAGITLKLTTSHFYPSVFVFHGGKHVLPSSAAPNLTRACNAARERFGFS------RCQ 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY. BELONGS TO THE HERPESVIRUSES DNA-BINDING PROTEIN
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                                                                                                                                                                                                                                                                                                                                            VALRVRNVTAVARGAAHLAFDENHEGAVLPPDITYTYFQSSSSGTTTARGARRNDVNSTS
                                                                                                                                                             RLNALGSYTARVAGVIGAMVFSPNSALYLTEVEDSGMTEAKDGGPGPSFNRFYQFAG---
                                                                                                                                                                                                                                                  KPSPSGGFERRLASIMAADT-ALHAEVIFNTGIYE---ETPTDIK--EWPMFIGMEGTLP 360
                                                                                                                                                                                                                                                                                                  QALRVRRVGKL - - - - -
                                                                                                                                                                                                                                                                                                                                                                                    DVIRIPLFFVQLFMPDVNRLVPDPFNTHHRSIGEGFVYPTPFYNTGLCHLIHDCVIAPMA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SKPGDFFPE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GPPVDGAVETTGAEICTRLGLEFENTILYLVVTALFKEAVFMCNVFLHYGGLDIVHINHG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DPNCGL---LRATSYHRDIYVFHNAHMVPPIFEGPGLEALCGETREVFGYDAYSALPRES 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GPCGYIYFYPLATYPLREVATLGTGYAGHRCLTVPLLCGITVEPGFSIN---VKALHRRP 74
                                                                    -----PHLAANPQTDRDGHVLSSQSTGSSNTEFSVDYLALICGFGAPLLARLLF
                                                                                                                 RVAALHRYNASLAPHVSTQIFATNSVLYV-----SGVSKSTGQGKESLFNSFYMTHGLGT
                                                                                                                                                                                                          ISHPDSG-----ALMIVDSAACELAVSYAPAMLEASHETPASLNYDSWPLFADCEGPEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----GLDPSAYLGAVAITEAFKERLYSGNLVAIPSLKQEVAVGQS 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 2.5e-43
                                                                                                                                                                                                                                                                                               ----VELLEKQSLQDQAKVAKVAPLKEFPAST
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                                                                                                Viruses; dsDNA viruses, no RNA stage; Gammaherpesvirinae; Rhadinovirus.
                                                                                                                                                                                                                      01 MAR 1992 (Rel. 2), Created)
01 MAR-1992 (Rel. 2), Last sequence up
16 OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                      ASASH
MEDIJINE-90163221; PubMed-2154888
                                                                                                                                                                            OF KEKEL
                                                                                                                                                                                              Major DNA-binding protein.
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                                                                                                                                                                                                                                                                                                                            DNH HSVSA
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                                                                      NCBI_TaxID-10383;
                                                                                                                                             Herpesvirus salmiri (strain 11)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1127 E 1127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1178 K 1178
                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                856 PRTQSVPARDYPHVLG TRAVESAA-----AYAEATSSLTAT-TVVCAATDCLSQVC 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 TTRRENYI INGPYMKFLNTYHKTLF - - - - PDTKLSSLYLWHNFSRRRSVPVPSGASA 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                690 PDLDAALQGRYYGKKLPVKMSKVLMLCPRNIKIKNRVVFTGENAALQNS-----FIKS 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  583 K NNITYKOLVKSCYHVMQYSCNPFAQPACPIFTQLFYRSLLTILQDISLPICMC---- 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              636 ETRIDYKTREGI.SEATHSMALTFIDPYSGAFCPTTNFLVKRTHLAVVQDLALSQCHCVFYGQ 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VRAVGARAQHMAFDDWLSLT - : DDEFLARDLEELHDQIIQTLET - - - - - PWTVEGALEA 1125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RKQAGGSSMRKKFYFATFFILGLTVKRRTQAATTYELENIRAGLEALLSQKQEEDCVFDVV 1015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KARPVVTLPVTINKYTGVNGNNQIFQAGN-LGYFMGRGV-----DRN---LLQAPGAGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EEYSDLALFYDOGSRAHEESNYLDYYPGNLYTYAKORLNNAILKACGOTQFYISLIQGLY 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EEITTIAA VKRETEEYAAINFINLPPTCIGELAQFYMANLILKYCDHSQYLINTLTSII 916
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QVEGRNERNQFQPVLRRREVDLENGGE----ISTRSITV----TLSEGPVSAPNPTLG- 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ERLSRLGIDAEGKLEKEPHGP - · -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGAPPPROPSSVI HWIPKDVTSAADIETQAKALLEKTENLPELWTTAFTSTHLVRAAM 974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - EGVWGGPGAAQUNE ISVAEPVSTASQASAGILLIGGGGGGGGGGGFRKRPLATVLPGL-1126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -YEND-NPGLGQSPPEWLKGHYQTLCTNERSLAIDKGVLTAKEAKVVHGEPTCDL 689
                                                                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FICPVTGPSSGNR-ETTLSDQVRGIIVSGGAMV-----QLAIYATV 1073
                                                                                                                                                                                                                                                Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------RDFVKMFKDVDAAVDAEVVQFMNSMA 582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 1128 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA-binding; DNA replication; Zinc-finger; Nuclear protein ZN_FING 453\,-466\, C2HC-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X64346; CAA45629.1; -. EMBL; M31122; AAA46162.1; -. EMBL; M60849; AAA46157.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensewisb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nicholas J., Coles L.S., Newman C., Honess R.W.; "Regulation of the herpesvirus saimiri (HVS) delayed-carly 110-kilodalton promoter by HVS immediate-early gene products and a homolog of the Epstein-Barr virus R trans activator."; J Virol 65.2457-2466(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Albrecht J.-C., Nicholas J., Biller D., Cameron K.R., Biesinger Newman C., Wittmann S., Craxton M.A., Coleman H., Fleckenstein E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Albrecht J.-C., Fleckenstein B.;
"Structural organization of the conserved gene block of Herpesvirus saimiri coding for DNA polymerase, glycoprotein B, and major DNA binding protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00747; viral_DNA_bp; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; G36806; DNBEM1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- FUNCTION: SINGLE-STRAND DNA-BINDING PROTEIN REQUIRED FOR DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-91202588; PubMed=1850023;
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Honess R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
260 ----DFSLQSVKCQDASAFMV1DC)AAELAMSYGLSFLEAPQDPCAVLDYTSWP1FETA 314
                                           310 PSGGFERRLASIMAADTA------LHAEVIFNTGI-YEETP -----TDIKEWPMFIGM 355
                                                                                                                               250 RVRNVTAVARGAAHLAFDENHEGAVLPPDITTYTYEQSSSSGTTTARGARRNDVNSTSKPS
                                                                                                                                                                            189 KIPLYDEDLFSKSHEHL-----
                                                                                                                                                                                                                                                                                                    131 DGAVETTGAEICTRLGLEPENTILYLVYTALFKEAVFMCN-VFLHYGGLDIVHINHGDVI 189
                                                                                                                                                                                                                                                                                                                                                                                                                                          18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 PTGPLGYVYACRVEDLDLEEISFLAARSTDSDLALLPLMRNLTVEKTFTSSLAVVSGART 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Virol. 66:5047-5058(1992).
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                                                                                   RIRDVESVIRASEKQSIQDQYKLAK) ---
                                                                                                                                                                                                                  RIPLEPPQLEMPDVNRLVPDPENTHHRSIGEGEVYPTPEYNTGLCHLIHDCVIAPMAVAL 249
                                                                                                                                                                                                                                                                                                                                               M-----TTLLVRVSAYHREAIVFFNTDLEEPIFVGPGLDILCSDARSLEGYTNF --VPR 129
                                                                                                                                                                                                                                                              TULKUTVUIKULYAPEYSEUSCEMAVVVIEGEKERLYEGNLVPIIAQGIK-VQINGREAV 188
                                                                                                                                                                                                                                                                                                                                                                                          TGLAGAGITLKLTTSHFYPSVFVFHGGKHVLPSSAAPNLTRACNAARERFGFSRCQGPPV 130
                                                                                                                                                                                                                                                                                                                                                                                                                                   PVEPCGYIYVYPKEGFPFKEASLLGNKNVGASAMSLPLLSDLTVESNFSFNVKAVHKKID 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.6%; Score 604; DB 1; ilarity 22:9%; Pred. No. 2.7e-38; Conservative 189; Mismatches 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127457 MW; BA3ADE86138132BD CRC64;
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                                                                                                                                                                       ----PRFYIPSVSKYLHDSVFTSIAQAL
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                                                                                                                                                                                                                01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                 Human herpesvirus (type 6 / strain Uganda-1102) (HHV6).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                    DNBI_HSV611
P52338;
MEDLINE-95266321; PubMed=7747482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1072 TV----VRAVGARAQHMAFDDWLSLTDDEFLARDLEELHDQIIQTLETPWTVEGALEAV 1126
                       SEQUENCE FROM N.A.
                                                                       NCHI_TaxID=10370;
                                                                                                 Betaherpesvirinae; Roseolovirus
                                                                                                                                                                                             Major DNA-binding protein (MDBP)
                                                                                                                                                                                                                                                                                                                                                                                                                                             1015 NVVLELVKGLGDSCENITEDDLQFYLGEYYIMSDEIWSRFQIITDSGAPWSVENVTKVL 1073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                751 YLVTGPYMKFLNSLHKVMF-----PNAKISALYLWHTFSQKKQLPVLPGISRENMVELAN 805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   601 YCCNVEWQAPCAMELNI.FYKSVLAIIQDICLPIAMTYEQDNPSIGMMPSEWLKVHY--QT 658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RÜNNSSYMRKKHYFMTPMYAHLVKKNSNLNNLTFEVETIRKNYQNIFEDKD---NLNIFD 1014
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TEYPHVLLDQSIMSVDHYLSSIKDKHALTVQTTLKEDIATVGK---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AVKRFTEEYAAINFINLPPTCIGELAQFYMANLILKYCDHSQYLINTLTSI-----ITG 918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTMNSQYSDCDPLGNYAPYLILRKPGDQTEAAKATMQDTYRATLERLFIDLEQEPLLDRG 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----QRPIVTVPLVVNKYTGINGNTQIFQCGNLGYFMGRGVDRNLIPDSTGFR 957
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA-binding; DNA replication; Zinc-finger; Nuclear protein ZN_FING 459 475 C4-TYPE.
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Pfam; PF00747; viral_DNA_bp; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 1132 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to liceuse@isb-sib.ch).
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                                            481 VRVGTRLPATPKNVKKEPLVMSMFSRYYAEVDILGSFG----RKPVSELKEIGKDQQNT 535
574 YRATLERLFIDLEGERLLDRGA-----PCSSEGLSSVIVDHPTFR-----RILDT 618
                                                                                                514 HRLRQRMPRFGQATRQPIGVFGTMNSQYSDCDPLGNYAPYLILRKPGDQTEAAKATMQDT 573
                                                                                                                                                                                                 454 CGFGAPLLARLLFYLERCDAGAFTGGHGDALKYVTGTFDSEIPCSLCEKHTRPVCAHTTV 513
                                                                                                                                                                                                                                                 370 SVMTQ-----ELLLRSLSFCNALSSLSDDVYNDNRKIIKCDSTSGKDDKFSANHLAYA 422
                                                                                                                                                                                                                                                                                                395 SGMTEAKDGGPGPSENRFYQFAGPHLAANPQTDRDGH-VLSSQSTGSSNTEFSVDYLALI 453
                                                                                                                                                                                                                                                                                                                                                  310 MNENDWPIIRNSETHAERMAQLTNLKLHLSSHLAVLIFAPNSILYCSKLAFIPNVKQAFN
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                                                                                                                                                  CATSPQLLSEVVWNLNRMSVYNAGNAHTEIYNHLVNC--SANLCEFCDGKCCQSCIGTAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCVEEQTQVQVGEYSCVKIPLYSATLEETE-----ETISLSSCTEFIQERGFFIPA 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LCHLIHDCVIAPMAVALRVRNVTAVARGAAHLAFDENHEGAVLPPDITYTYFQSSSSGTT 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAVVSGARTTGLAGAGITLKLTTSHFYPSVFVFHGGKHVL-PSSAAPNLTRACNAARERF 120
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                                                                                                                                                                                                                                                                                                                                                                                                 ---KEWPMFIGMEGTLPRLNALGSYTARVAGVIGAMVFSPNSALYLTEVE------D
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21.8%; Pred. No. 1.2
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This SWISS PROF entry is copyright, it is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way.
                                                                                                                                                                                                                                                                                                                                                    suggests acquisition of ority) by transposition J. Virol. 69:589-596(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01 oct 1996 (Rel. 34, Created)
01 oct 1996 (Rel. 34, Last sequence update)
16 oct 2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                      Stamey F.R., Dominquez G., Black J.B., Dambaugh T.R., Pellett P.E., "Intragenomic linear amplification of human herpesvirus 6B orityt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Major DNA binding protein (MDBP).
U41 OK KAZI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI TaxID-36351;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viruses, dsDNA viruses, no RNA stage, Herpesviridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human herpesvirus (type 6 / strain 229) (HHV6).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDILINE 95074921; PubMed-7983761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1066 NHILVDMNVKDESIT NIGSVEETVSSNDAPVYDESEILAEEDDQGNGVLKCDETET 1120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             945 QAKALLEKTENLPELWTTAFTSTHLVRAAMNQRPMVVLGISISKYHGAAGNNRVFQAG-- 1002
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                                                                                                                                                                                                                                                                                                                   FUNCTION: SINGLE STRAND DNA-BINDING PROTEIN REQUIRED FOR DNA
                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE HERPESVIRUSES DNA-BINDING PROTEIN
                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Nuclear (Probable)
                                                                                                                                                                                                                                                                                      REPLICATION.
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Pfam; PF00747; viral_DNA_bp; 1.
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                              771 VKNRVVFSGNCTNLSEAARARLVGLASAYQRQEKRVDMLHGALGFLLKQFHGLLFPRGMP 830
                                                                                        684 KGFLNTRTVKV------ASNVDMEQILDCDLYKSGKYVKITIQAKLCKLSMQCLRDFR 735
                                                                                                                                                                                                                                                                                                                                                                                                                                            526 KETGKDQQNTLS--------LURGKFYSQTFUYCKKNSLTDPYTGEDTFNYRS 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    504 TRPVCAHTTVHRLRQRMPRFGQATRQPIGVFGTMNSQYSDCDPLGNYAPYLILKKPGDQT 563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                370 SVMTQ-----ELLLRSLSFCNALSSLTEDVYNDNRKIIKCDSTSGKDDKFSANHLAYA 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          395 SGMTEAKDGGPGPSFNRFYQFAGPHLAANPQTDRDGH-VLSSQSTGSSNTEFSVDYLALI 453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 HLQSFEVFTARKVIDIKA--LCSAVGKDADSVICHVACGNGFKELLF------AGLLI 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 V-----KTPITNFGGTILTKITSFMPVCFFFHGTEQLVGMAEDHGDLIRLCEQTRQKF 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 LAVVSGARTTGLAGAGITLKLTTSHFYPSVFVFHGGKHVL-PSSAAPNLTRAGNAARERF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 ENTOKTVTVPTGPLGYVYACRVEDLDLEELSELAARSTDSDLALLPLMRNLTVEKTETSS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCQSCIGTAMVPVGTPLPAIPKNVKKEPLVMSMFSPYYAEVPILGSFG-----FKFVSEL 525
                                                                                                                                               GGFISTRSITVTLSEGPVSAPNPTLGQ--DA---PAGR----TFDGDLARVSVEVIRDIR 770
                                                                                                                                                                                                          LTFAYYKVILTVLQNLAL----IVASGHVVDRPCTGNSISKWLVQQYQSLYGTFHSSYLK 683
                                                                                                                                                                                                                                                                 TNFLVKRTHLAVVQDLALSQCHCVFYGGGVEGRNERNQEQEVLKKKEVDLE------N-719
                                                                                                                                                                                                                                                                                                                              KKDFVSIIHGLTQCIEECVS---RCIVEMKKTQTEREQIENCLQSENVDTTTYATAFSET 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MNFNDWPITRNSETHAERMAQLTNLKLHLSSHLAVLIFAPNSILYCSKLAFIPNVKQAFN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EAAKATMQDTYRATLERLFIDLEQERLLDRGA-----PCSSEGLSSVIVDHPTFR--- 613
                                                                                                                                                                                                                                                                                                                                                                                     -----RILDTLRARIEQTTTQFMKVLVETRDYKI-REGLSEATHSMALTFDPYSGAFCPI 667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----FLMLVDSVV-TELSFSHVAEYLDSVYD--PSQI 309
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     Query Match
Best Local Similarity
Matches 258; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P52339;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation updat
                                                                                                                          InterPro; IPR000635; Viral_DNA_bind.

Pfam; PF90747, viral_DNA_bp; 1.

DNA-binding; DNA replication; Zinc-finger; Nuclear protein.

ZN_FING 459 475 C2HC-TYPE.
                                                                                                                                                                                                                          EMBL; U43400; AAC54703.1;
                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
-:- FUNCTION: SINGLE-STRAND DNA-BINDING PROTEIN REQUIRED FOR DNA
REPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nicholas J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=JI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human herpesvirus (type 7 / strain JI) (HHV7).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Major DNA-hinding protein (MDBP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNBI_HSV7J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1056 ALAASIMLKINHIVUMNVRDFSIA-NIQSVFEAVSSNDAPVYDFSEILAEEDDQASGVIK 1114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1097 FLARD-----LEELHDQIIQTLETPWTVEGALEAV------------KILDEKTTAGDG---- 1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alphaherpesvirinae; Simplexvirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Nuclear (Probable).
SIMILARITY: BELONGS TO THE HERPESVIRUSES DNA-BINDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NREYFQFGQLGWIGGSGVDRNLNPTSSALQDFRFMR-QKTIIATKFSEVIV-----KKVR 998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NNRVFQAG--NWSGLNG-GKNVCPL-----FTFDRTRRFIIACPRGGFICPVTGPSSGN 1045
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                                                                                                  1131 AA;
  Conservative
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                    7.7%; Score 483; DB 1; Length 1131; 20.8%; Pred. No. 6.4e-29;
                                                                                                  129008 MW;
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Mismatches
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                  913 SLTKEPNFGSIFTGRS11TrGLM1EKFVSVASRDYFHFGQLGW1AGSGVDRNLNPPSSGL 972
                                                              963 AFTSTHLVRAAMNQRPMVVLGISISKYHGAAGNN--RVFQAGNWSGLNGGKNVCPL---- 1016
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                                                                                                                                                                 907 YL--INTLISIITGARRPRDPSSVLHWIRKDYT--SAADIETQAKALLEKTENLPELWTT 962
                                                                                                                                                                                                                                                            850 MP--ADKLTHEEITT IAAVKRFTEEYAAINFINLPPTCIGELAQFYMANLILKYCDHSQ 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          627 TTQFMKVLVETRDYKIREGLSEATHSMALTFDPYSGAFCPITNFLVKRTHLAVVQDLALS 686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           542 K ----- FLGMIHDY ----- CKKNNLIDAITGEDNLNFKSQNDFVNMINDLIQCIEEA 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          575 RATLERLFIDLEQERLLDRGAPCSSEGLSSVIV--DHPTFR-----RILDTLRARIEOT 626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           589 VSKCISEMRKTQ--TSREQIENCLQSFNIDTTPLSLAFSPFFVFTYYKVILIVLQNLAL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           345 DIKEWPMFIGMEGTLPRLNALGSYTARVAGVIGAMVFSPNSALYLTEVEDSGMTEAKDGG
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                                                                                                                                                                                                                MPKTIDIGNVEDMRSFIKFTFRVTNSYDEIDLLDIQPECLLSFIEYYFHNKLLSVLGYKD
                                                                                                                                                                                                                                                                                                                                                            ARLVGLASAYQRQEKRVDMLHGALGFLLKQFHGLLFPRGMPPNSKSPNPQWFWTLLQRNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APNPTLGQ------DAPAGRTFDGDLARVSVEVIRDIRVKNRVVFSGNCTNLSEAAR 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---IIGTGYVVDRPCTGNLISKWLMQQYQSLYGAFYNSHFKKGFLNMKTVKI------
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                                                                                                               YLTSLHALTSKLV----PQNPMLFPVFLKEHPTFSSVQEYVMHVKKLV--GNGLKEPMTA 912
                                                                                                                                                                                                                                                                                                                                                                                                                ASNVDMEQYIDFNLFKSGKYAKTSIQAKLCRLSMQCLKDFRVKNRPFNKPNKNTQNN----
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                                                                                                                                                                                                                                                                                                                -----PFFKKVKQKKNPLSGCLSFLLFKYHERLF----PNLKISCLE-FWQRILLNN 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --QAFNSAITQETLLRSIQFCNSLSSLNEDFYNDARKLIKCNSSPCKEDKFSAFHLAYAC
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                                                                                                    Best becal Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       *Location, transcript analysis, and partial nucleotide sequence of
the cytomegalovirus gene encoding an early DNA-binding protein with
similarities to ICPB of herpes simplex virus type 1.*;
                                                                                                                                                                                                                                                   InterPro: (PR000635; Viral_DNA_bind.
Pfam; PF00747; viral_DNA_bp; 1.
                                                                                                                                                                                                                                                                                                            EMBL; D00750; BAA00647.1; EMBL; M19868; AAA46066.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Nucleotide sequence of a cytomegalovirus single-stranded DNA-binding protein dene: comparison with alpha—and gammaherpesvirus counterparts reveals conserved segments.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Simian cytomegalovirus (Strain Colburn)
Viruses; debna viruses, no PNA stage; H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PISITS;
PISITS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMVO
                                                                                                                                                                  SEQUENCE 1160 AA:
                                                                                                                                                                                                                                                                                               PIR: A36256; A36256.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ULS / OR DBP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Major DNA binding protein (MDBP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01 APR 1993 (Rel. 25, Last sequence update)
16 oct 2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1084 FEEQVEDSAAIYDESELLVEGNEQGEGILKCEETEHENEEPS 1125
                                                                                                                                                                                                         Early protein
                                                                                                                                                                                                                           DNA binding; DNA replication; Zine-tinger; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                              or send an email to licensewish sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anders D.G., Gibson W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDILINE-88155776; PubMed-2831398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anders D.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDILINE-91037979; PubMed-2172458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCB1 Tax10~50292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Betaberpesvirinae: Cytomegalovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01 JAN 1990 (Rel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1027 LILLIAEVMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1067 LAIYATTVKAVGARAQHMAFDDWLSLTDD-EFLARDLE-----ELHDQIIQTLETP 1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 205-308 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9/3 QUEREMR-QKEVIATK----LCDII-VKKVKREAIVYDVEVIRGKVLNIIESLSNSVNPE 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gen. Virol. 71:2451 2456(1990)
                                     1 MENTOKTVTVPTGPLGYVYACKVEDLDLEEISFLAAKSTDSDLALLPLMRNLTVEKTFTS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VITOL: 62:1364-1372(1988).
FUNCTION: SINGLE-STRAND DNA-HINDING PROTEIN REQUIRED FOR DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCALION: Nuclear (Probable).
SIMILARITY: BELONGS TO THE HERPESVIRUSES DNA-BINDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPLICATION.
MSNEELSALAPVGPAAYVYETKTNHEMNEVLATLSLCDSSSPVVIAPLLMGLTVDQDECT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FTFDRTRRFILACPRGGF1CPVTGPSSGNRETTLSD--QVRG11-----VSGGAMVQ-1066
                                                                                 Conservative
                                                                                                                                                                                          465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      · DROSKPTMDDMLFYVDGREPLAKSVMNKIQHLTDLNVHDFSLSTLLSV 1083
                                                                                                                                                                                        479
                                                                                                    7.6%; Score 479.5;
21.3%; Pred. No. 1.2
                                                                                                                                                                129005 MW: 7037716816974B1A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -TVEGALEAVKILDEKTTAGDGETPT 1142
                                                                                 202;
                                                                                                    Pred. No. 1.2c=28;
                                                                                                                                                                                        CZHC TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                 Mismutches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Herpesviridae;
                                                                                                                      DH 1; Length 1160;
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Дb
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                                                       1002 GN---WSG-----LN----GGKNVCPLETEDRTRRFITACPRGGFICPVTGPSSGNRET 1048
970 GQIGYESGNGVERSLNTNSIGGQD----YKEMK-QRCILAFKLSDVL1-----KKSRRDN 1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   700
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                                                                                                                                                                                942 IETQAKALLEKTENLPELWTTAFTSTHLVRAAMNQRPMVVLGISISKYHGAAGNNRVFQA 100
                                                                                                                                                                                                                                                 854 DCMLNYLENRFHNKFLCFYGFKDYIGTLHGLTTRLTYQNHAQFP--YILGESPNFASAAD 911
                                                                                                                                                                                                                                                                                                                                                                                                                                  831 PNSKSPNPQWFWTLLQRNQMPADKLTHEEITTIAAVKRF-----TEEYAAINFINLPP 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           773 NRVVFSGNCTNLSEAARARLVGLASAYORQE--KRVDMLHGALGFLLKQFHGLIFPRGMP 830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           592 FINLYSSLNKFYDDEAMSFYS---EVRMKSNRDEVLGATQAFNLDLNPFAVSFSPILAYE 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             672 VKFTHLAVVQULALS;:"H"VFYGQ----gvegenefnqfqfvflkkkfydlfnggflstrs 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  351 MFIGMEGTLPRLNALGSYTARVAGV1GAMVFSPNSAL-----YLTEVEDSGMTEAKDGG 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 YAIESYM--PEEGRAPTDLAALCTAAGCDPQEVLVHVVVGNGMKEEMYAGQLIPCFEEAA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 SLAVVSGARTTGLAGAGITLKLTTSHFYPSVFVFHGGKHVLP-SSAAPNLTRACNAARER 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTRINDCDAVRVPLYPPTLFGSLQADVD---SDELSLDKKS---SFVESBCLYVPAVSET 225
                                                                                                                     FALRLKDL - - KATGYTAPLASTYTRESLMRTIFEQRSLYTYSESIEKYAGYNNNKETYQF
                                                                                                                                                                                                                                                                                                                                                                          --DCGFSCLQFWQKVCANALP----KNVNLGUMGEFNNFVKFVLSVTADYNEHDL1DVPP-85:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----RKGFLFIRNVKSSKNADHDRLPDFKLYARGTYSVISMEIKLSRLSVPSLLMFRVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YYRVIFAIIQNVALITATSYIVDNPLTTSLVSRWVTQHFQS1------HGAFSTTSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRRILDTLRARIEQTTTQFMKVLVETRDYKIREGLSEATHSMALTFDPYSGAFCPTTNFL 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NTAFVRVQTRLPQMPRLPKKEPSVVVMQSRFLNDVDVLGTFG----RRYSAESKEASLDA 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HTTVHRLRQRMPRFGQATRQPIGVFGTMNSQYSDCDPLGNYAPYLILRKPGDQTEA----- 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FIWYLNRVSV------YNTGLTGSSTLSNHLIGCSSSLCGACGGTCCHT---CY 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ILEYLERCDAGAFTGGHGDALKYVTGTFDSE-----IPC--SLCEK-----HTRPVCA 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PGPSENREYQFAGPHLAANPQTDRDGH-VLSSQSTGSSNTEFSVDYLALICGFGAPLLAR 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IVHINHGDVIRIPLFPVQLF---MPDVNRLVPDPFNTHHRSIGEGFVYPTPFYNTGLCHL 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FGFSRCQGPPVDGAVETTGAE1CTRLGLEPENT1LYLVVTALFKEAVFMCNVF1HYGGLD 179
                                                                                                                                                                                                                                                                                                            TCIGELAQEYMANLICKYCDHSQYI -- INTLTSITTGARRPRDPSSVLHWIRKEVTSAAD 941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NRP1----SKASKGT---TAHVFFRREHVPKKNPVKGCLGFLLYKYHDKLFP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KADEGSASTSNRTASSSVDRTHR--LNRILDYCKKMRLID-----SVTGEDTMTINGRSD 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SQEVILKSIHFANGLTGLCEDTYNDARKLIKCSGVVAKDERYAPYHLSLICGTCPQLFSA 4 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----LSSLEKD-----HIMLSDAVICELGESFASVFLDSAYGASDSMVYSEWP 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARRNDVNSTSKPSPSGGFERRLASIMAADTAL-----HAEVIENTGIYEETPTDIKEWP 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LFYYVYTSWCQALRFSETKVLIEAALKQFVNDSQQSVKLAPHKKYFGYTSQK------- 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SV-----RTPVVCYDGGVLTKVTS-FCPFALYFYNTQGIVDFSEPHGDVQRLCDETRQR 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ITVTLSEGPVSAPNPTLGQDAPAGR ------TFDGDLARVSVEV(RD)RVK 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VVVNATDHRDLTRALTELKI.HI.STHTSALLESCNSTLYHNRLVYLTSNKNASGT-----GA 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IHDCVIAPMAVALRVRNVTAVARGAAHLAFDENHEGAVLPPDITYTYFQSSSSGTTTARG 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --AKATMQDTYRATLERLFIDLEQERLLDRGAPCSSEGLSSVIVD-HPT 611
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Db	ζ	Db	Ç,	Db	Qу
1118 DLSALFTAASGEAVGNSV-GLNARGGEHAFDEDCGLLPAKRGRL 1160	1156 DTTSNVLNISGSNISGSTVPGLK-RPPEDDELFDLSGIPIKHGNI 1199	1073 QAVADSLMEKESRLQEMGVDDFSLVNLQQVLDSRPECGGGGGEVH 1117	1096 EFLARDLEELHDQIIQTLETPWTVEGALEAVKILDEKTTAGDGETPTNLAFNFDSCEPSH 1155	1020 VLFDEDIIKNRVMAALDSENLDVDPELMAMYEILSTREEIPERDDVLFFVDGC 1072	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

Search completed: March 28, 2003, 13:36:03 Job time : 37 secs

